

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 06:53:17 ; Search time 38.7949 Seconds
(without alignments)
456.424 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKA AVLTLAVLFLTGSQARH.....SPKVSFLSALBEYTKKLNLTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
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| 1 | 1362 | 100.0 | 267 | 1 | US-07-959-946-3 |
| 2 | 1362 | 100.0 | 267 | 1 | US-08-333-577-3 |
| 3 | 1362 | 100.0 | 267 | 3 | US-08-952-796-2 |
| 4 | 1362 | 100.0 | 267 | 4 | US-08-940-136-260 |
| 5 | 1362 | 100.0 | 267 | 5 | PCT-US92-08634-3 |
| 6 | 1346 | 98.8 | 267 | 4 | US-09-919-039-27 |
| 7 | 1241 | 91.1 | 243 | 4 | US-09-079-030-119 |
| 8 | 1240.5 | 91.1 | 264 | 1 | US-08-448-606-6 |
| 9 | 1006 | 73.9 | 200 | 3 | US-08-952-796-15 |
| 10 | 328 | 24.1 | 64 | 2 | US-08-292-870-1 |
| 11 | 278.5 | 20.4 | 396 | 4 | US-09-800-729-207 |
| 12 | 269 | 19.8 | 382 | 4 | US-09-800-729-206 |
| 13 | 251 | 18.4 | 391 | 4 | US-09-800-729-208 |
| 14 | 229.5 | 16.9 | 397 | 4 | US-09-079-030-123 |
| 15 | 227 | 16.7 | 44 | 2 | US-08-292-870-2 |
| 16 | 200 | 14.7 | 366 | 4 | US-09-750-580-3 |
| 17 | 200 | 14.7 | 366 | 4 | US-09-599-360B-89 |
| 18 | 198 | 14.5 | 363 | 4 | US-09-800-729-111 |
| 19 | 198 | 14.5 | 366 | 4 | US-09-800-729-212 |
| 20 | 190 | 14.0 | 317 | 3 | US-08-949-155-6 |
| 21 | 190 | 14.0 | 317 | 3 | US-09-819-964-6 |
| 22 | 174.5 | 12.8 | 316 | 4 | US-09-919-039-247 |
| 23 | 171.5 | 12.6 | 317 | 1 | US-07-709-949-2 |
| 24 | 163 | 12.0 | 32 | 2 | US-08-292-870-3 |
| 25 | 147.5 | 10.8 | 239 | 4 | US-09-108-006C-62 |
| 26 | 145 | 10.6 | 242 | 4 | US-09-543-681A-5933 |
| 27 | 133.5 | 9.8 | 1972 | 4 | US-08-875-435B-3 |

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| 28 | 131 | 9.6 | 579 | 4 | US-09-538-092-1284 | Sequence 1284, Ap |
| 29 | 131 | 9.6 | 585 | 4 | US-09-462-951B-1 | Sequence 1, Appli |
| 30 | 131 | 9.6 | 1530 | 4 | US-09-976-594-736 | Sequence 736, App |
| 31 | 130 | 9.5 | 1201 | 4 | US-09-252-991A-32259 | Sequence 32259, A |
| 32 | 129.5 | 9.5 | 977 | 4 | US-09-010-147B-18 | Sequence 18, Appl |
| 33 | 129 | 9.5 | 900 | 2 | US-08-630-822A-62 | Sequence 62, Appl |
| 34 | 129 | 9.5 | 900 | 2 | US-09-005-069-62 | Sequence 62, Appl |
| 35 | 129 | 9.5 | 900 | 3 | US-09-171-156A-21 | Sequence 21, Appl |
| 36 | 129 | 9.5 | 900 | 4 | US-09-004-730A-21 | Sequence 21, Appl |
| 37 | 129 | 9.5 | 900 | 4 | US-08-981-799A-21 | Sequence 21, Appl |
| 38 | 128.5 | 9.4 | 1976 | 4 | US-09-538-092-1078 | Sequence 1078, Ap |
| 39 | 127.5 | 9.4 | 691 | 4 | US-10-140-002-16 | Sequence 16, Appl |
| 40 | 126 | 9.3 | 220 | 2 | US-08-726-306A-29 | Sequence 29, Appl |
| 41 | 126 | 9.3 | 718 | 4 | US-09-540-236-2753 | Sequence 2753, Ap |
| 42 | 126 | 9.3 | 1935 | 4 | US-09-538-092-916 | Sequence 916, App |
| 43 | 125.5 | 9.2 | 1078 | 4 | US-09-248-796A-20284 | Sequence 20284, A |
| 44 | 124 | 9.1 | 25 | 2 | US-08-292-870-4 | Sequence 4, Appli |
| 45 | 123.5 | 9.1 | 683 | 6 | 5210183-3 | Patent No. 5210183 |

ALIGNMENTS

RESULT 1
US-07-959-946-3
; Sequence 3, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-946-3

Query Match 100.0%; Score 1362; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 7.1e-109;

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| | | | | | | | | | | |
| Db | 1 | MKAAVLT | LAVLFLTGSQARHF | WQDEPPQSPWDRVK | LATVYVDVLKDSGRD | VYSQFEGS | 60 | | | |
| | | | | | | | | | | |
| QY | 61 | ALGKQLNL | KLLDNWD | SVTSTFSKLR | EQLGPTQEF | FDNLEK | TEGLRQEMSKD | LEEVKAK | 120 | |
| | | | | | | | | | | |
| Db | 61 | ALGKQLNL | KLLDNWD | SVTSTFSKLR | EQLGPTQEF | FDNLEK | TEGLRQEMSKD | LEEVKAK | 120 | |
| | | | | | | | | | | |
| QY | 121 | VQPYLDD | FQKKWQ | EEMLYRQK | VEPLRAELQ | EGARQKLHE | LQEKLSPLGE | EMRDRARAHV | 180 | |
| | | | | | | | | | | |
| Db | 121 | VQPYLDD | FQKKWQ | EEMLYRQK | VEPLRAELQ | EGARQKLHE | LQEKLSPLGE | EMRDRARAHV | 180 | |
| | | | | | | | | | | |
| QY | 181 | DALRTHL | APYSDEL | RQRLAAR | LEALKENG | GARLA | EYHAKATE | HLSTLSEKAK | PALEDLRQ | 240 |
| | | | | | | | | | | |
| Db | 181 | DALRTHL | APYSDEL | RQRLAAR | LEALKENG | GARLA | EYHAKATE | HLSTLSEKAK | PALEDLRQ | 240 |
| | | | | | | | | | | |
| QY | 241 | GLLPVLE | SFKVSFL | SALEEYTK | KLNTQ | 267 | | | | |
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| Db | 241 | GLLPVLE | SFKVSFL | SALEEYTK | KLNTQ | 267 | | | | |
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RESULT 2
US-08-333-577-3
; Sequence 3, Application US/08333577
; Patent No. 5786206
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,577
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 234.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-333-577-3

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| Db | 1 | MKAAVLTLAVLFTGSOARHFQQDEPPQSPWDRVKDLATVYVDVLKQ |
| QY | 61 | ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGRLQ |
| Db | 61 | ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGRLQ |
| QY | 121 | VQPYLDDFQKQWQEMELYRQKVEPLRAELOEGARQKLHELQEKLSPL |
| Db | 121 | VQPYLDDFQKQWQEMELYRQKVEPLRAELOEGARQKLHELQEKLSPL |
| QY | 181 | DALRTHLAPYSDELQRQLAARLEALKKENGARLAAYHAKATEHLSTLS |
| Db | 181 | DALRTHLAPYSDELQRQLAARLEALKKENGARLAAYHAKATEHLSTLS |
| QY | 241 | GLLPVLESFKVSFLSALEEYTKKLNTQ 267 |
| Db | 241 | GLLPVLESFKVSFLSALEEYTKKLNTQ 267 |

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RESULT 3
US-08-952-796-2
; Sequence 2, Application US/08952796
; Patent No. 6258596
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: BRUCKERT, Eric
; APPLICANT: DENEFLÉ, Patrice
; APPLICANT: DUBERGER, Nicolas
; APPLICANT: FRUCHART, Jean-Charles
; APPLICANT: LUC, Gerald
; APPLICANT: TURPIN, Gerard
; APPLICANT: ASSMANN, Gerd
; APPLICANT: FUNKE, Harald
; TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,796
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/06061
; FILING DATE: 22-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR96/00747
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlnér Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95031-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-952-796-2

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; MOLECULE TYPE: protein
PCT-US92-08634-3

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QY    61  ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEE VKAK 120
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QY    121 VQPYLDDDFQKKWQEEMELYRQKVPEPLRAELQEGARQKHLEQEKLSPLGEEMRDRARA HV 180
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Db    121 VQPYLDDDFQKKWQEEMELYRQKVPEPLRAELQEGARQKHLEQEKLSPLGEEMRDRARA HV 180
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QY    181 DALRTHLPYSDEL RQLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALED LRQ 240
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Db    181 DALRTHLPYSDEL RQLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALED LRQ 240
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QY    241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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Db    241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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RESULT 6
 US-09-919-039-27
 ; Sequence 27, Application US/09919039
 ; Patent No. 6727066
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 27
 ; LENGTH: 267
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6727066 2516070CD1
 US-09-919-039-27

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| | | Query Match | 98.8%; Score 1346; DB 4; | Length 267; |
| | | Best Local Similarity | 98.9%; Pred. No. | 1.7e-107; |
| | | Matches 264; Conservative | 1; Mismatches 2; | Indels 0; Gaps 0; |
| QY | 1 | MKAAVLT LAVFLTGSQA RHFQQDEPPQPSPWDRVKDLATVVVDVLKDSGRDVS QFEGS | 60 | |
| Dd | 1 | MKAAVLT LAVFLTGSQA RHFQQDEPPQPSPWDRVKDLATVVVDVLKDSGRDVS QFEGS | 60 | |
| QY | 61 | ALGKQLNL KLLDNWDSVTSPFSKLREQ LGPVTQE FWDNLEKETEGLRQEMS KOLEEVKA K | 120 | |
| Dd | 61 | ALGKQLNL KLLDNWDSVTSPFSKLREQ LGPVTQE FWDNLEKETEGLRQEMS KOLEEVKA K | 120 | |
| QY | 121 | VQPYLDDFQKKWQEEMEL YRKVEPLRAELQEGAROKLHELQEKLS PLGEEMRD RAHV | 180 | |
| Dd | 121 | VQPYLDDFQKKWQEEMEL YRKVEPLRAELQEGAROKLHELQEKLS PLGEEMRD RAHV | 180 | |
| QY | 181 | DALRTH LAPYSDELQR LAARLEALKENG GARLA EYHAKATEHLSTLSEKAK PALEDLRQ | 240 | : |
| Dd | 181 | ARVRTH LAPYSDELQR LAARLEALKENG GARLA EYHAKATEHLSTLSEKAK PALEDLRQ | 240 | |
| QY | 241 | G LLPVLESFKVS FL SALLEEYTK KLNTQ | 267 | |

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Db          241  GLLPVLESFKVSFLSALEEYTKKLNTQ  267

RESULT 7
US-09-079-030-119
; Sequence 119, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.
; APPLICANT: Hoogeveen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,030
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: ARAG:003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-030-119

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Query Match      91.1%; Score 1241; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.4e-98;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 84
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QY 85 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFKKKWQEEEMELYRQKVE 144
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Db 61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFKKKWQEEEMELYRQKVE 120
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QY 145 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEA 204
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Db 121 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEA 180
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QY 205 LKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKL 264
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Db 181 LKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKL 240
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QY 265 NTQ 267
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Db 241 NTQ 243

RESULT 8
US-08-448-606-6
; Sequence 6, Application US/08448606

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; Patent No. 5721114
; GENERAL INFORMATION:
; APPLICANT: Abrahams n, Lars
; APPLICANT: Holmgren, Erik
; APPLICANT: Kalder n, Christina
; APPLICANT: Lake, Mats
; APPLICANT: Mikaelsson, sa
; APPLICANT: Sejlitz, Torsten
; TITLE OF INVENTION: Expression System For Producing
; TITLE OF INVENTION: Apolipoprotein AI-M
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pollock, Vande Sande & Priddy
; STREET: 1990 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,606
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE93/01061
; FILING DATE: 09-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203753-0
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Amernick, Burton A.
; REGISTRATION NUMBER: 24,852
; REFERENCE/DOCKET NUMBER: 0151/00121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)331-7111
; TELEFAX: (202) 293-6229
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-448-606-6

Query Match 91.1%; Score 1240.5; DB 1; Length 264;
Best Local Similarity 92.2%; Pred. No. 1.8e-98;
Matches 249; Conservative 3; Mismatches 9; Indels 9; Gaps 2;
QY 1 MKA AVLTLAVL---FLTGSQARHFQQDEPPQSPWDRVKOLATVYVDVLKDSGRDYVSQF 57
Db 1 MKKTAIAIAVALAGFATVANA-----DEPPQSPWDRVKOLATVYVDVLKDSGRDYVSQF 54
QY 58 EGSALGKQLNLKLLDNWDSVTSTFSKLRQLGPTVQEFWDNLEKETETGLRQEMSKDLEEV 117
Db 55 EGSALGKQLNLKLLDNWDSVTSTFSKLRQLGPTVQEFWDNLEKETETGLRQEMSKDLEEV 114
QY 118 KAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRAR 177
Db 115 KAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRAR 174
QY 178 AHVDALRTHLAPYSDELQRQLAARLEALKENGGARLAEBYHAKATEHLSTLSEKAKPALED 237
Db 175 AHVDALRTHLAPYSDELQRQLAARLEALKENGGARLAEBYHAKATEHLSTLSEKAKPALED 234
QY 238 LRQGLLPVLESFKVSFLSALEEYTKKLNTQ 267
Db 235 LRQGLLPVLESFKVSFLSALEEYTKKLNTQ 264

RESULT 9
US-08-952-796-15
; Sequence 15, Application US/08952796
; Patent No. 6258596
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: BRUCKERT, Eric
; APPLICANT: DENEFE, Patrice
; APPLICANT: DUBERGER, Nicolas
; APPLICANT: FRUCHART, Jean-Charles
; APPLICANT: LUC, Gerald
; APPLICANT: TURPIN, Gerard
; APPLICANT: ASSMANN, Gerd
; APPLICANT: FUNKE, Harald
; TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,796
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/06061
; FILING DATE: 22-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR96/00747
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlnr Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95031-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-952-796-15
Query Match 73.9%; Score 1006; DB 3; Length 200;
Best Local Similarity 99.5%; Pred. No. 1.5e-78;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 68 LKLLDNWDSVTSTFSKLRQLGPTVQEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLDD 127
Db 1 LKLLDNWDSVTSTFSKLRQLGPTVQEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLDD 60
QY 128 FQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHL 187
Db 61 FQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDCARAHVDALRTHL 120
QY 188 APYSDELQRQLAARLEALKENGGARLAEBYHAKATEHLSTLSEKAKPALEDLRQGLLPVLE 247
Db 121 APYSDELQRQLAARLEALKENGGARLAEBYHAKATEHLSTLSEKAKPALEDLRQGLLPVLE 180
QY 248 SFKVSFLSALEEYTKKLNTQ 267
Db 181 SFKVSFLSALEEYTKKLNTQ 200

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 06:40:58 ; Search time 32.2747 Seconds
(without alignments)
795.975 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKA AVLTLAVLFLTGSQARH.....SPKVSFLSALEEYTKLNTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------|--------------------|
| 1 | 1362 | 100.0 | 267 | 1 | LPHUA1 | apolipoprotein A-I |
| 2 | 1306 | 95.9 | 267 | 2 | JS0079 | apolipoprotein A-I |
| 3 | 1299 | 95.4 | 267 | 1 | A26529 | apolipoprotein A-I |
| 4 | 1161.5 | 85.3 | 266 | 1 | LPDGA1 | apolipoprotein A-I |
| 5 | 1100.5 | 80.8 | 266 | 1 | LPRB1Z | apolipoprotein A-I |
| 6 | 1100 | 80.8 | 265 | 2 | A46018 | apolipoprotein AI |
| 7 | 1093 | 80.2 | 265 | 2 | JT0672 | apolipoprotein A-I |
| 8 | 1087.5 | 79.8 | 264 | 2 | S31394 | apolipoprotein A-I |
| 9 | 1082 | 79.4 | 265 | 1 | LPRB1B | apolipoprotein A-I |
| 10 | 1082 | 79.4 | 265 | 2 | A56858 | apolipoprotein A-I |
| 11 | 974.5 | 71.5 | 241 | 2 | A24998 | apolipoprotein A-I |
| 12 | 924 | 67.8 | 231 | 2 | JQ0704 | apolipoprotein A-I |
| 13 | 904.5 | 66.4 | 264 | 2 | S22420 | apolipoprotein A-I |
| 14 | 898.5 | 66.0 | 262 | 2 | JC1237 | apolipoprotein A-I |
| 15 | 849.5 | 62.4 | 259 | 2 | A24700 | apolipoprotein A-I |
| 16 | 688.5 | 50.6 | 264 | 1 | LPCHA1 | apolipoprotein A-I |
| 17 | 663.5 | 48.7 | 264 | 2 | JC5456 | apolipoprotein A-I |
| 18 | 644.5 | 47.3 | 246 | 2 | A61448 | apolipoprotein A-I |
| 19 | 617.5 | 45.3 | 164 | 2 | S21830 | apolipoprotein A-I |
| 20 | 291 | 21.4 | 429 | 2 | S29565 | apolipoprotein A-I |
| 21 | 278.5 | 20.4 | 396 | 1 | LPHUA4 | apolipoprotein A-I |
| 22 | 267 | 19.6 | 391 | 1 | LPRTA4 | apolipoprotein A-I |
| 23 | 253 | 18.6 | 399 | 2 | C40892 | apolipoprotein A-I |
| 24 | 251 | 18.4 | 391 | 2 | B40892 | apolipoprotein A-I |
| 25 | 251 | 18.4 | 395 | 2 | A40892 | apolipoprotein A-I |
| 26 | 249.5 | 18.3 | 401 | 2 | A47141 | apolipoprotein A-I |
| 27 | 238.5 | 17.5 | 394 | 2 | A25281 | apolipoprotein A-I |
| 28 | 225.5 | 16.6 | 258 | 2 | JH0472 | apolipoprotein A-I |
| 29 | 209 | 15.3 | 311 | 2 | JU0036 | apolipoprotein E p |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 30 | 198 | 14.5 | 312 | 1 | LPRTE | apolipoprotein E p |
| 31 | 194.5 | 14.3 | 1547 | 2 | T28657 | blackjack protein, |
| 32 | 190.5 | 14.0 | 317 | 2 | A28792 | apolipoprotein E p |
| 33 | 189.5 | 13.9 | 317 | 2 | S03185 | apolipoprotein E p |
| 34 | 188 | 13.8 | 317 | 2 | S33450 | apolipoprotein E - |
| 35 | 184 | 13.5 | 298 | 2 | S12635 | apolipoprotein E p |
| 36 | 182 | 13.4 | 329 | 2 | JC5566 | apolipoprotein E p |
| 37 | 178.5 | 13.1 | 291 | 2 | C60940 | apolipoprotein E - |
| 38 | 174.5 | 12.8 | 317 | 1 | LPHUE | apolipoprotein E p |
| 39 | 166.5 | 12.2 | 316 | 2 | JC6549 | apolipoprotein E p |
| 40 | 160 | 11.7 | 316 | 2 | I45996 | apolipoprotein E - |
| 41 | 160 | 11.7 | 316 | 2 | S26478 | apolipoprotein E - |
| 42 | 147 | 10.8 | 311 | 2 | A45951 | apolipoprotein E p |
| 43 | 146 | 10.7 | 513 | 2 | S08381 | keratin, 58K type |
| 44 | 143.5 | 10.5 | 771 | 1 | A33430 | h-caldesmon - chic |
| 45 | 137 | 10.1 | 470 | 2 | T23512 | hypothetical prote |

ALIGNMENTS

RESULT 1
LPHUA1
apolipoprotein A-I precursor [validated] - human
N;Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor
C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 09-Jul-2004
C;Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; A2
6197
R;Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.
DNA 3, 309-317, 1984
A;Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for huma
A;Reference number: A90947; MUID:85026665; PMID:6207999
A;Accession: A90947
A;Molecule type: DNA
A;Residues: 1-267 <SE1>
A;Cross-references: UNIPROT:P02647; GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
A;Accession: B90947
A;Molecule type: mRNA
A;Residues: 1-267 <SE2>
A;Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
R;Makrides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis, V.
Eur. J. Biochem. 173, 465-471, 1988
A;Title: Sequence and expression of Tangier apoA-I gene.
A;Reference number: S02373; MUID:88196137; PMID:3129297
A;Accession: S02373
A;Molecule type: DNA
A;Residues: 1-267 <MAK>
A;Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729
R;Shoulders, C.C.; Kornblihtt, A.R.; Munro, B.S.; Baralle, F.E.
Nucleic Acids Res. 11, 2827-2837, 1983
A;Title: Gene structure of human apolipoprotein A1.
A;Reference number: A93465; MUID:83220822; PMID:6406984
A;Accession: A93465
A;Molecule type: DNA
A;Residues: 1-267 <SHO>
A;Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:X01518; G.
R;Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983
A;Title: Isolation and characterization of the human apolipoprotein A-I gene.
A;Reference number: A21147; MUID:84016011; PMID:6413973
A;Accession: A21147
A;Molecule type: DNA
A;Residues: 1-267 <KAR>
A;Cross-references: GB:J00098; GB:J03222; NID:g178765; PIDN:AAB59514.1; PID:g178768
R;Sharpe, C.R.; Sidoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.E.
Nucleic Acids Res. 12, 3917-3932, 1984
A;Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundance
A;Reference number: A93519; MUID:84221405; PMID:6328445
A;Accession: A93519
A;Molecule type: mRNA
A;Residues: 1-267 <SHA>
A;Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

A;Accession: B93519
A;Molecule type: DNA
A;Residues: 1-24 <SH2>
R;Cheung, P.; Chan, L.
Nucleic Acids Res. 11, 3703-3715, 1983
A;Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
A;Reference number: A93472; MUID:83220772; PMID:6304641
A;Accession: A93472
A;Molecule type: mRNA
A;Residues: 1-267 <CHE>
A;Cross-references: GB:J00098; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB
R;Law, S.W.; Brewer Jr., H.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
A;Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
A;Reference number: A94010; MUID:84119464; PMID:6198645
A;Accession: A94010
A;Molecule type: mRNA
A;Residues: 1-267 <LAW>
A;Cross-references: GB:J00098; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB
R;Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
A;Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
A;Reference number: A21118; MUID:83195100; PMID:6405383
A;Accession: A21118
A;Molecule type: mRNA
A;Residues: 1-24 <ZAN>
R;Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Ronan, R.; Law, S.; Light, J.A.
Biochem. Biophys. Res. Commun. 113, 626-632, 1983
A;Title: Human plasma proapo-A-I: isolation and amino-terminal sequence.
A;Reference number: A90112; MUID:83256553; PMID:6409108
A;Accession: A90112
A;Molecule type: protein
A;Residues: 19-27 <BRE>
R;Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Ronan, R.; Houser, A.; Bronzert, T.J.
Biochem. Biophys. Res. Commun. 80, 623-630, 1978
A;Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high d
A;Reference number: A90209; MUID:78123731; PMID:204308
A;Accession: A90209
A;Molecule type: protein
A;Residues: 25-57,'Q',59-169,'QQ',172-267 <BR2>
R;Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
J. Clin. Invest. 82, 803-807, 1988
A;Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A
A;Reference number: A30516; MUID:88331387; PMID:3047170
A;Accession: A30516
A;Molecule type: protein
A;Residues: 25-56 <YUI>
R;Nichols, W.C.; Dwulet, F.E.; Liepnieks, J.; Benson, M.D.
Biochem. Biophys. Res. Commun. 156, 762-768, 1988
A;Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
A;Reference number: A31582; MUID:89050104; PMID:3142462
A;Accession: A31582
A;Molecule type: protein
A;Residues: 25-49,'R',51-85,'D',87-107 <NIC>
A;Note: variant sequence from patient with familial amyloidotic polyneuropathy type III
R;Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.
J. Biol. Chem. 264, 16853-16857, 1989
A;Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
A;Reference number: A34409; MUID:89380318; PMID:2506184
A;Accession: A34409
A;Molecule type: protein
A;Residues: 25-48 <MAN>
R;Stoffel, W.; Binczek, E.
Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
A;Title: Structural requirements of human preproapolipoprotein AI for translocation and
A;Reference number: S02737; MUID:89149957; PMID:3228490
A;Accession: S02737
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-6,'AV',9,'LV',12-29 <STO>
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Stoffel, W.; Binczek, E.
Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A;Title: Transient expression of wild type and mutant human apolipoprotein AI in COS cel
A;Reference number: S16197; MUID:92029676; PMID:1930731
A;Contents: annotation; extension of studies in reference S02737
R;Stoffel, W.; Kruger, E.; Deutzmann, R.
Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
A;Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processing
A;Reference number: A19913; MUID:83236195; PMID:6407957
A;Accession: B19913
A;Molecule type: protein
A;Residues: 1-6,'X',8-13,'XXX',17-18,'XX',21,'X',23-25,'X',27-29 <ST2>
R;Ehnholm, C.; Bozas, S.E.; Tenkanen, H.; Kirszbaum, L.; Metso, J.; Murphy, B.; Walker,
Biochim. Biophys. Acta 1086, 255-260, 1991
A;Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein of
A;Reference number: A56815; MUID:92075698; PMID:1742316
A;Accession: A56815
A;Molecule type: protein
A;Residues: 25-31,'p',33 <EHN>
A;Experimental source: serum
A;Note: sequence extracted from NCBI backbone (NCBIP:69759)
A;Note: 32-Trp was also found
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
A;Reference number: A54223; MUID:94162201; PMID:8117655
A;Accession: A54223
A;Molecule type: protein
A;Residues: 25-39 <KUN>
R;Mogulevsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.; He
DNA 8, 429-436, 1989
A;Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: puri
A;Reference number: I39476; MUID:89377481; PMID:2673706
A;Accession: I39476
A;Molecule type: mRNA
A;Residues: 19-267 <RES>
A;Cross-references: GB:M29068; NID:gl78774; PIDN:AAA51747.1; PID:gl78775
R;Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
J. Biol. Chem. 263, 18530-18536, 1988
A;Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the S
A;Reference number: I39475; MUID:89054040; PMID:3142880
A;Accession: I39475
A;Molecule type: DNA
A;Residues: 1-14 <RE2>
A;Cross-references: GB:J04066; NID:gl78763; PIDN:AAA51746.1; PID:g553183
R;Breslow, J.L.
Annu. Rev. Biochem. 54, 699-727, 1985
A;Title: Human apolipoprotein molecular biology and genetic variation.
A;Reference number: A90042; MUID:85278004; PMID:3896129
A;Contents: annotation; review of sequences, variants and gene location
R;Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.
J. Biol. Chem. 261, 3911-3914, 1986
A;Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acylat
A;Reference number: A92577; MUID:86140194; PMID:3005308
A;Contents: annotation; acylation with palmitate
A;Note: an undetermined serine or threonine is acylated by fatty acid; the acylating fat
R;Law, S.W.; Brewer, H.B.
J. Biol. Chem. 260, 12810-12814, 1985
A;Title: Tangier disease: The complete mRNA sequence encoding for preproapo-A-I.
A;Reference number: I55236; MUID:86008382; PMID:2995392
A;Accession: I55236
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-143,'D',145-267 <RE3>
A;Cross-references: GB:M11791; NID:gl78776; PIDN:AAA35545.1; PID:gl78777
C;Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine
coteins (HDL) in plasma.
C;Genetics:
A;Gene: GDB:APOA1
A;Cross-references: GDB:119684; OMIM:107680
A;Map position: 11q23.3-11q23.3
A;Introns: 15/1; 67/2
C;Function:
A;Description: participates in the reverse transport of cholesterol from tissues to the
sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2)

C;Superfamily: apolipoprotein A-I
C;Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipid
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-267/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 100.0%; Score 1362; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.3e-69;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVFLTGSQARHFVQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60
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Db 1 MKA AVLTLAVFLTGSQARHFVQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLR EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
|||
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLR EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
QY 121 VQPYLDDFQKKWQEE MELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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Db 121 VQPYLDDFQKKWQEE MELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
QY 181 DALRTHLAPYSDELQRQLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240
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Db 181 DALRTHLAPYSDELQRQLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GLLPVLESFKVSFLSAL E EYTKKLN TQ 267
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Db 241 GLLPVLESFKVSFLSAL E EYTKKLN TQ 267

RESULT 2
JS0079
apolipoprotein A-I precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Jun-1997
C;Accession: JS0079
R;Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; VandeBerg, J.L.
Gene 74, 483-490, 1988
A;Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and id
A;Reference number: JS0079; MUID:89232739; PMID:2907746
A;Accession: JS0079
A;Molecule type: mRNA
A;Residues: 1-267 <HIX>

A;Experimental source: liver
C;Comment: This protein is the principal protein component of high density lipoprotein p
C;Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase co
C;Comment: This protein contains a region of repeated amino acids which form amphipathic
C;Genetics:
A;Gene: apoAI
C;Superfamily: apolipoprotein A-I
C;Keywords: HDL; lipid binding; lipoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-267/Product: apolipoprotein A-I #status predicted <LAI>
F;123-144,145-166,167-188,189-210,211-232,233-254/Region: tandem repeats

Query Match 95.9%; Score 1306; DB 2; Length 267;
Best Local Similarity 95.1%; Pred. No. 4.4e-66;
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVFLTGSQARHFVQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60
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Db 1 MKATVLTAVFLTGSQARHFVQQDEPPQTPWDRVKDLVTVYVEALKDSGKDYSQFE GS 60
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLR EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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Db 61 ALGKQLNLKLLDNWDSVTSTFSKLR EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
QY 121 VQPYLDDFQKKWQEE MELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
|||
Db 121 VQPYLDDFQKKWQEE MELYRQKVEPLRAELHEGTRQKLHELHEKLSPLGEEVRDRARAHV 180
QY 181 DALRTHLAPYSDELQRQLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELQRQLAARLEALKENG GARLA EYHAKASEHLSLSEKAKPALEDLRQ 240
QY 241 GLLPVLESFKVSFLSAL E EYTKKLN TQ 267
Db 241 GLLPVLESFKVSFLSAL E EYTKKLN STQ 267
RESULT 3
A26529
apolipoprotein A-I precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 30-Sep-1989 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A26529; A26627; S23135; A57766
R;Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marotti, K.R.
Gene 49, 103-110, 1986
A;Title: The primary structure of cynomolgus monkey apolipoprotein A-1 deduced from the
A;Reference number: A26529; MUID:87191989; PMID:3106152
A;Accession: A26529
A;Molecule type: mRNA
A;Residues: 1-267 <POL>
A;Cross-references: UNIPROT:P15568; GB:M15411; NID:g342074; PIDN:AAA36834.1; PID:g34207
R;Herbert, P.N.; Bausserman, L.L.; Lynch, K.M.; Saritelli, A.L.; Kantor, M.A.; Nicolosi
Biochemistry 26, 1457-1463, 1987
A;Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (cy
A;Reference number: A26627; MUID:87185451; PMID:3105581
A;Accession: A26627
A;Molecule type: protein
A;Residues: 25-48 <HER>
R;Murray, R.W.; Marotti, K.R.
Biochim. Biophys. Acta 1131, 207-210, 1992
A;Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and corre
A;Reference number: S23135; MUID:92305062; PMID:1610902
A;Accession: S23135
A;Molecule type: DNA
A;Residues: 1-12,'L',14-267 <MUR>
A;Cross-references: GB:M83242; NID:g342070; PIDN:AAA36832.1; PID:g342071
R;Sorci-Thomas, M.; Kearns, M.W.
J. Biol. Chem. 266, 18045-18050, 1991
A;Title: Transcriptional regulation of the apolipoprotein A-I gene.
A;Reference number: A57766; MUID:92011532; PMID:1917942
A;Accession: A57766
A;Molecule type: DNA
A;Residues: 1-10 <RES>
A;Cross-references: GB:M69223; NID:g342066; PIDN:AAA36831.1; PID:g553820
C;Comment: The precursor is synthesized in the liver and small intestine. The propeptid
C;Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins (H
Y promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin
C;Genetics:
A;Introns: 15/1; 67/2
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem rep
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PPT>
F;25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 95.4%; Score 1299; DB 1; Length 267;
Best Local Similarity 94.8%; Pred. No. 1.1e-65;
Matches 253; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVFLTGSQARHFVQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60
|||
Db 1 MKATVLTAVFLFPTGSQARHFVQQDEPPTPWDRVKDLVTVYVEALKDSGKDYSQFE GS 60
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLR EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
|||
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLR EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
QY 121 VQPYLDDFQKKWQEE MELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
|||
Db 121 VQPYLDDFQKKWQEE MELYRQKVEPLRAELHEGTRQKLHELHEKLSPLGEEVRDRARAHV 180
QY 181 DALRTHLAPYSDELQRQLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKASEHLSTLSEKAKPALEDLRQ 240
QY 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLSTQ 267

RESULT 4
LPDGA1
apolipoprotein A-I precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 17-Dec-1982 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A60940; A03092; A61418
R;Luo, C.C.; Li, W.H.; Chan, L.
J. Lipid Res. 30, 1735-1746, 1989
A;Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implicati
A;Reference number: A60940; MUID:90132271; PMID:2515239
A;Accession: A60940
A;Molecule type: mRNA
A;Residues: 1-266 <LUO>
A;Cross-references: UNIPROT:P02648
R;Chung, H.; Randolph, A.; Reardon, I.; Heinrikson, R.L.
J. Biol. Chem. 257, 2961-2967, 1982
A;Title: The covalent structure of apolipoprotein A-I from canine high density lipoprote
A;Reference number: A03092; MUID:82142425; PMID:6801039
A;Accession: A03092
A;Molecule type: protein
A;Residues: 25-167,'G',169-201,'Q',203-234,'Q',236-266 <CHU>
R;Nakai, T.; Whayne, T.F.; Tang, J.
FEBS Lett. 64, 409-411, 1976
A;Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.
A;Reference number: A61418; MUID:76210910; PMID:179887
A;Accession: A61418
A;Molecule type: protein
A;Residues: 25-56,'Z',261-262,'A' <NAK>
C;Superfamily: apolipoprotein A-I
C;Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; li
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 85.3%; Score 1161.5; DB 1; Length 266;
Best Local Similarity 85.0%; Pred. No. 4.8e-58;
Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKA AVLTLAVLFTGTSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKA ALLTLAVLFTGTSQARHFQQDE-PQSPWDRVKDLATVYVDVAVKDSGRDYVAQFEAS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
Db 60 ALGKQLNLKLLDNWDSLSSTVTKLREQIGPVTQEFWDNLEKETEVLRQEMSKDLEEVKQK 119

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db 60 ALGKQLNLKLLDNWDSLSSTVTKLREQIGPVTQEFWDNLEKETEVLRQEMSKDLEEVKQK 119

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db 120 VQPYLDDFQKKWQEMELYRQKVAPLGSELREGARQKLQELQEKLSPLAEELRDRARTHV 179

QY 181 DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 DALRAQLAPYSDDLRLERLAARLEALKEGGGASLAEYHARASEQLSALGEKARPALEDLRQ 239

QY 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 240 GLLPVLESFKVSLAAIDEATKKLNAQ 266

RESULT 5
LPRB1Z
apolipoprotein A-I precursor (clone 2Zap AI) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S06064

R;Paraskevopoulou, T.B.; Kritis, A.; Zannis, V.
submitted to the EMBL Data Library, July 1989
A;Reference number: S06064
A;Accession: S06064
A;Molecule type: mRNA
A;Residues: 1-266 <PAR>
A;Cross-references: UNIPROT:P09809; EMBL:X15908; NID:g1457; PIDN:CAA34024.1; PID:g1458
C;Comment: This protein is synthesized in the small intestine.
C;Comment: This protein is a major component of the high density lipoproteins in plasma.
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem rep
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 80.8%; Score 1100.5; DB 1; Length 266;
Best Local Similarity 80.1%; Pred. No. 1.2e-54;
Matches 214; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

QY 1 MKA AVLTLAVLFTGTSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKA VVTLAVLFTGTSQARHFQQDE-PRSSWDKIKDFATVYVDVTKDSGREYVAQFEAS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
Db 60 AFGKQLNLKLLDNWDSLSSTVSKLQELGPVTQEFWDNLEKETEGRLREEMNKDQLEVRQK 119

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db 120 VQPYLDDFQKKWQEEVERYRQKVEPLGAELRESARQKLTELQEKLSPLAEELRDSARTHV 179

QY 181 DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 DTLRTKLAPYSNELQORLAARLESIKEGGASLAEYQAKAREHLSVLSEKARPALEDLRQ 239

QY 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 240 GLLPVLESFKASVQNVLDEATKKLNTQ 266

RESULT 6
A46018
apolipoprotein AI - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46018
R;Birchbauer, A.; Knipping, G.; Juritsch, B.; Aschauer, H.; Zechner, R.
Genomics 15, 643-652, 1993
A;Title: Characterization of the apolipoprotein AI and CIII genes in the domestic pig.
A;Reference number: A46018; MUID:93224154; PMID:8468059
A;Accession: A46018
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-265 <BIR>
A;Cross-references: UNIPROT:P18648; GB:L00626; NID:g164358; PIDN:AAA30992.1; PID:g164359
A;Note: sequence extracted from NCBI backbone (NCBIN:129509, NCBIIP:129511)
C;Superfamily: apolipoprotein A-I

Query Match 80.8%; Score 1100; DB 2; Length 265;
Best Local Similarity 80.9%; Pred. No. 1.3e-54;
Matches 216; Conservative 19; Mismatches 30; Indels 2; Gaps 2;

QY 1 MKA AVLTLAVLFTGTSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKA VVTLAVLFTGTSQARHFQQDD-PQSPWDRVKDFATVYVDAIKDSGRDYVAQFEAS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
Db 60 ALGKHLNLKLLDNWDSLSGSTFTKVRQLGPVTQEFWDNLEKETEARLQEMSKDLEEVKKK 119

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db 120 VQPYLDDFQKNKQWEMETRYRQKVAPLGAELFREGARQKVQELQEKLSPLAEELRDLRAHV 179

| | | | |
|--|-----|--|-----|
| Best Local Similarity 79.4%; Pred. No. 1.3e-53; | | Matches 212; Conservative 26; Mismatches 27; Indels 2; Gaps 2; | |
| QY | 1 | MKAAVLT LAVLFGTSQARHFHQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS | 60 |
| Db | 1 | MKAVVLT LAVLFGTSQARHFHQORDE-PRSSWDKIKDFATVYVDTVKDSGREYVAQFEAS | 59 |
| QY | 61 | ALGKQLNLKLLDNWDSVTSTFSKLRQQLPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 |
| Db | 60 | AFGKQLNLKLLDNWDSLSTSVSKLQEQLGPTQEFWDNLEKETEGLRQEMNKDLQEVROK | 119 |
| QY | 121 | VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV | 180 |
| Db | 120 | VQPFLEDFQKKWQEEEVERYRQKVEPLGAELGESARQKLTQLQEKLSPLAEELRDSARTHV | 179 |
| QY | 181 | DALRTHLAPYSDELQRQRLAARLEALKENGSGARLAEYHAKATEHLSLSEKAKPALEDLRQ | 240 |
| Db | 180 | DTLRTKLAPYSNEL-QRLAARLESIKEGGAKLAEYQAKAREHLSVLSEKARPALEDLRQ | 238 |
| QY | 241 | GLLPVLESFKVSFLSALEEYTKKLNTQ | 267 |
| Db | 239 | GLLPVLESFKASVQNVVDEATKKLNTQ | 265 |
| RESULT 10 | | | |
| A56858 | | | |
| apolipoprotein A-I precursor - bovine | | | |
| C;Species: Bos primigenius taurus (cattle) | | | |
| C;Date: 05-Jan-1996 #sequence revision 23-Aug-1997 #text_change 09-Jul-2004 | | | |
| C;Accession: I45853; A56858; A34649 | | | |
| R;O'Huigin, C.; Chan, L.; Li, W. | | | |
| Mol. Biol. Evol. 7, 327-339, 1990 | | | |
| A;Title: Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolution | | | |
| A;Reference number: I45853; MUID:90348478; PMID:2117227 | | | |
| A;Accession: I45853 | | | |
| A;Status: preliminary; translated from GB/EMBL/DBJ | | | |
| A;Molecule type: mRNA | | | |
| A;Residues: 1-265 <OXH> | | | |
| A;Cross-references: UNIPROT:P15497; GB:M35870; NID:g162677; PIDN:AAA30381.1; PID:g162678 | | | |
| R;Sparrow, D.A.; Lee, B.R.; Laplaud, P.M.; Auboirion, S.; Bauchart, D.; Chapman, M.J.; Gou | | | |
| Biochim. Biophys. Acta 1123, 145-150, 1992 | | | |
| A;Title: Plasma lipid transport in the preruminant calf, Bos spp: primary structure of b | | | |
| A;Reference number: A56858; MUID:92153895; PMID:1739745 | | | |
| A;Accession: A56858 | | | |
| A;Status: preliminary | | | |
| A;Molecule type: protein | | | |
| A;Residues: 19-184,'QL',187-265 <SPA> | | | |
| A;Experimental source: Friesian-Holstein male calves aged 2-4 weeks | | | |
| A;Note: sequence extracted from NCBI backbone (NCBIP:83520) | | | |
| R;Auboirion, S.; Sparrow, D.A.; Beaubatie, L.; Bauchart, D.; Sparrow, J.T.; Laplaud, P.M. | | | |
| Biochem. Biophys. Res. Commun. 166, 833-839, 1990 | | | |
| A;Title: Characterization and amino-terminal sequence of apolipoprotein AI from plasma h | | | |
| A;Reference number: A34649; MUID:90147795; PMID:2105728 | | | |
| A;Accession: A34649 | | | |
| A;Molecule type: protein | | | |
| A;Residues: 25-70 <AUB> | | | |
| A;Experimental source: Friesian-Holstein male calves aged 2-4 weeks | | | |
| C;Superfamily: apolipoprotein A-I | | | |
| C;Keywords: lipid binding; lipoprotein | | | |
| F;1-18/Domain: signal sequence #status predicted <SIG> | | | |
| F;19-265/Product: apolipoprotein A-I #status experimental <MAT> | | | |
| Query Match | | 79.4%; Score 1082; DB 2; Length 265; | |
| Best Local Similarity | | 78.7%; Pred. No. 1.3e-53; | |
| Matches 210; Conservative 24; Mismatches 31; Indels 2; Gaps 2; | | | |
| QY | 1 | MKAAVLT LAVLFGTSQARHFHQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS | 60 |
| Db | 1 | MKAVVLT LAVLFGTSQARHFHQDD-PQSSWDRVKDFATVYVEATKDSGRDYVAQFEAS | 59 |
| QY | 61 | ALGKQLNLKLLDNWDSVTSTFSKLRQQLPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 |
| Db | 60 | ALGKQLNLKLLDNWDTLASTLSKVRQQLPGVTQEFWDNLEKETASLRQEMHKDLEEVKQK | 119 |

| | | | |
|----|-----|--|-----|
| QY | 121 | VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV | 180 |
| Db | 120 | VQPYLDEFQKKWHEEVEIYRQKVAPLGEEFREGARQKVQELQDKLSPLAQELRDRARAHV | 179 |
| QY | 181 | DALRTHLAPYSDELQRQRLAARLEALKENGSGARLAEYHAKATEHLSLSEKAKPALEDLRQ | 240 |
| Db | 180 | ETLRQHVAPYSDDLQRQLRTARLEALKKEGGGS-LAEYHAKASEQLKALGEKAKPVLEDLRQ | 238 |
| QY | 241 | GLLPVLESFKVSFLSALEEYTKKLNTQ | 267 |
| Db | 239 | GLLPVLESCLKVSILAAIDEASKKLNAQ | 265 |

RESULT 11
A24998
apolipoprotein A-I - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-1993
C;Accession: A24998
R;Yang, C.; Yang, T.; Pownall, H.J.; Gotto Jr., A.M.
Eur. J. Biochem. 160, 427-431, 1986
A;Title: The primary structure of apolipoprotein A-I from rabbit high-density lipoprotein
A;Reference number: A24998; MUID:87030294; PMID:3095115
A;Accession: A24998
A;Molecule type: protein
A;Residues: 1-241 <YAN>
C;Superfamily: apolipoprotein A-I
C;Keywords: HDL; lipid binding; lipoprotein

Query Match 71.5%; Score 974.5; DB 2; Length 241;
Best Local Similarity 78.5%; Pred. No. 1.1e-47;
Matches 190; Conservative 23; Mismatches 28; Indels 1; Gaps 1;
QY 26 EPPQSPWDRVKOLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLR 85
Db 1 DEPRSSWDKIKDFATVYVDV-KDSGREYVAQFEASAFGKQLNLKLLDNWDSLSSTVSKLQ 59

QY 86 EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEP 145
Db 60 EQLGPVTQEFWDNLEKETEGLRQEMNKDLQEVROKQVQPYLDEFQKKWQEEEVERYRQKVEP 119
QY 146 LRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEAL 205
Db 120 LGVELRESARQKLTQLQEKLSPLAEELRDSARTHVDTLRTKLAPYSQELQQLAARLESI 179
QY 206 KENGGAARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLN 265
Db 180 KEGGASLAEYQAKAREHLSVLSEKARPALEDLRQGLLPVLESFKASVQNLVDEATKKLN 239
QY 266 TQ 267
Db 240 TQ 241

RESULT 12
JQ0704
apolipoprotein A-I - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Oct-1994
C;Accession: JQ0704
R;Weiler-Guettler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mischek, U.; Bonitz, D.; J
J. Neurochem. 54, 444-450, 1990
A;Title: Synthesis of apolipoprotein A-1 in pig brain microvascular endothelial cells.
A;Reference number: JQ0704; MUID:90132667; PMID:2105375
A;Accession: JQ0704
A;Molecule type: mRNA
A;Residues: 1-231 <WEI>
A;Note: the authors translated the codon CAG for residue 124 as His and GAC for residue
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein; p
Query Match 67.8%; Score 924; DB 2; Length 231;

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OM protein - protein search, using sw model
Run on: December 21, 2004, 07:13:28 ; Search time 157.462 Seconds
(without alignments)
975.635 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKAAVLTFLAVLFTGSQARH.....SPKVSFLSALEEYTKKLNQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | | |
|------------|--------|-------------|--------|-------|-------------|---------------------|
| Result No. | Score | Query Match | Length | DB ID | Description | |
| 1 | 1362 | 100.0 | 267 | 1 | APAI_HUMAN | P02647 homo sapien |
| 2 | 1362 | 100.0 | 267 | 2 | AAQ91811 | Aaq91811 homo sapi |
| 3 | 1362 | 100.0 | 267 | 2 | AAS68227 | Aas68227 homo sapi |
| 4 | 1306 | 95.9 | 267 | 1 | APAI_MACFA | P15568 macaca fasc |
| 5 | 1281 | 94.1 | 249 | 2 | Q6LDN9 | Q6ldn9 homo sapien |
| 6 | 1281 | 94.1 | 249 | 2 | AAA51747 | Aaa51747 homo sapi |
| 7 | 1161.5 | 85.3 | 266 | 1 | APAI_CANFA | P02648 canis famil |
| 8 | 1105 | 81.1 | 265 | 1 | APAI_PIG | P18648 sus scrofa |
| 9 | 1100.5 | 80.8 | 266 | 1 | APAI_RABIT | P09809 oryctolagus |
| 10 | 1077 | 79.1 | 265 | 1 | APAI_BOVIN | P15497 bos taurus |
| 11 | 1012.5 | 74.3 | 264 | 2 | Q9Z2L4 | Q9z2l4 mesocricetu |
| 12 | 975.5 | 71.6 | 265 | 1 | APAI_TUPGB | O18759 tupaiia glis |
| 13 | 962 | 70.6 | 191 | 2 | Q8HZ96 | Q8hz96 gorilla gor |
| 14 | 962 | 70.6 | 191 | 2 | Q8HZ97 | Q8hz97 pan troglod |
| 15 | 947 | 69.5 | 191 | 2 | Q8HZ95 | Q8hz95 pongo pygma |
| 16 | 905.5 | 66.5 | 264 | 2 | Q8BPD5 | Q8bpd5 mus musculu |
| 17 | 904.5 | 66.4 | 264 | 1 | APAI_MOUSE | Q00623 mus musculu |
| 18 | 896 | 65.8 | 263 | 2 | O08855 | O08855 mus musculu |
| 19 | 895 | 65.7 | 263 | 2 | O09042 | O09042 mus musculu |
| 20 | 842.5 | 61.9 | 259 | 1 | APAI_RAT | P04639 rattus norv |
| 21 | 836 | 61.4 | 258 | 2 | O09054 | O09054 rattus norv |
| 22 | 834 | 61.2 | 258 | 2 | O08877 | O08877 rattus norv |
| 23 | 823 | 60.4 | 191 | 2 | Q8HZ94 | Q8hz94 saguinus oe |
| 24 | 727.5 | 53.4 | 241 | 2 | Q9TS49 | Q9ts49 erinaceus e |
| 25 | 705.5 | 51.8 | 264 | 1 | APAI_ANAPL | O42296 anas platyr |
| 26 | 688.5 | 50.6 | 264 | 1 | APAI_CHICK | P08250 gallus gall |
| 27 | 663.5 | 48.7 | 264 | 1 | APAI_COTJA | P32918 coturnix co |
| 28 | 526 | 38.6 | 260 | 2 | Q7ZYS5 | Q7zy85 xenopus lae |
| 29 | 519 | 38.1 | 260 | 2 | Q7SZA1 | Q7szal xenopus lae |
| 30 | 512 | 37.6 | 261 | 2 | Q6DDC5 | Q6ddc5 xenopus tro |
| 31 | 327 | 24.0 | 67 | 2 | Q9Y355 | Q9y355 homo sapien |

| ALIGNMENTS | | | | | | |
|------------|--|-----------|------|---------|--|--|
| RESULT 1 | | | | | | |
| APAI_HUMAN | APAI_HUMAN | STANDARD; | PRT; | 267 AA. | | |
| ID | APAI_HUMAN | STANDARD; | PRT; | 267 AA. | | |
| AC | P02647; | | | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | | | |
| DT | 01-OCT-2004 (Rel. 45, Last annotation update) | | | | | |
| DE | Apolipoprotein A-I precursor (Apo-AI). | | | | | |
| GN | Name=APOA1; | | | | | |
| OS | Homo sapiens (Human). | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | | |
| OX | NCBI_TaxID=9606; | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=84221405; PubMed=6328445; | | | | | |
| RA | Sharpe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C., | | | | | |
| RA | Baralle F.E.; | | | | | |
| RT | "Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA | | | | | |
| RL | abundance."; | | | | | |
| RL | Nucleic Acids Res. 12:3917-3932(1984). | | | | | |
| RN | [2] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=85026665; PubMed=6207999; | | | | | |
| RA | Seilhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.; | | | | | |
| RT | "Isolation and DNA sequence of full-length cDNA and of the entire gene | | | | | |
| RT | for human apolipoprotein AI -- discovery of a new genetic polymorphism | | | | | |
| RT | in the apo AI gene."; | | | | | |
| RL | DNA 3:309-317(1984). | | | | | |
| RN | [3] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=83220822; PubMed=6406984; | | | | | |
| RA | Shoulders C.C., Kornblihtt A.R., Munro B.S., Baralle F.E.; | | | | | |
| RT | "Gene structure of human apolipoprotein AI."; | | | | | |
| RL | Nucleic Acids Res. 11:2827-2837(1983). | | | | | |
| RN | [4] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=83220772; PubMed=6304641; | | | | | |
| RA | Cheung P., Chan L.; | | | | | |
| RT | "Nucleotide sequence of cloned cDNA of human apolipoprotein A-I."; | | | | | |
| RL | Nucleic Acids Res. 11:3703-3715(1983). | | | | | |
| RN | [5] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=84119464; PubMed=6198645; | | | | | |
| RA | Law S.W., Brewer H.B. Jr.; | | | | | |
| RT | "Nucleotide sequence and the encoded amino acids of human | | | | | |
| RT | apolipoprotein A-I mRNA."; | | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984). | | | | | |
| RN | [6] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=86008382; PubMed=2995392; | | | | | |
| RA | Law S.W., Brewer H.B. Jr.; | | | | | |
| RT | "Tangier disease. The complete mRNA sequence encoding for preproapo-A- | | | | | |
| RT | I."; | | | | | |

Q6ld50 mus sp. apo
Aab35539 mus sp. a
Q29248 sus scrofa
Q6p7h6 xenopus lae
Aah61667 xenopus l
Q6pbbs xenopus lae
Aah59786 xenopus l
Q98tg6 anguilla ja
P33621 macaca fasc
Q6dhe2 brachydanio
O42363 brachydanio
P06727 homo sapien
Aaq91809 homo sapi
Aas68228 homo sapi

RL J. Biol. Chem. 260:12810-12814(1985).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=84016011; PubMed=6413973;
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
RT "Isolation and characterization of the human apolipoprotein A-I
RT gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=89377481; PubMed=2673706;
RA Moguilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Bollen A.;
RT "Production of human recombinant proapolipoprotein A-I in Escherichia
RT coli: purification and biochemical characterization.";
RL DNA 8:429-436(1989).
RN [9]
RP SEQUENCE FROM N.A. (VARIANT TANGIER).
RX MEDLINE=88196137; PubMed=3129297;
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
RA Zannis V.I.;
RT "Sequence and expression of Tangier apoA-I gene.";
RL Eur. J. Biochem. 173:465-471(1988).
RN [10]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP SEQUENCE OF 118-267 FROM N.A.
RX MEDLINE=83091059; PubMed=6294659;
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
RT "Isolation and characterization of cDNA clones for human
RT apolipoprotein A-I.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
RN [12]
RP SEQUENCE OF 19-27.
RX MEDLINE=83256553; PubMed=6409108;
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Ronan R., Law S.,
RA Light J.A.;
RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
RN [13]
RP SEQUENCE OF 25-267.
RX MEDLINE=78123731; PubMed=204308;
RA Brewer H.B. Jr., Fairwell T., Larue A., Ronan R., Houser A.,
RA Bronzert T.J.;
RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated
RT from high density lipoproteins.";
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
RN [14]
RP SEQUENCE OF 25-267.

RX MEDLINE=75133493; PubMed=164450;
RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;
RT "The primary structure of human plasma high density apolipoprotein
RT glutamine I (ApoA-I). II. The amino acid sequence and alignment of
RT cyanogen bromide fragments IV, III, and I.";
RL J. Biol. Chem. 250:2725-2738(1975).
RN [15]
RP SEQUENCE OF 25-56.
RX MEDLINE=88331387; PubMed=3047170;
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein
RT A-I (Apo A-I). A novel function of Apo A-I.";
RL J. Clin. Invest. 82:803-807(1988).
RN [16]
RP SEQUENCE OF 25-48.
RX MEDLINE=89380318; PubMed=2506184;
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
RA Chapdelaine A.;
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
RT proteins.";
RL J. Biol. Chem. 264:16853-16857(1989).
RN [17]
RP SEQUENCE OF 25-43.
RX MEDLINE=88070603; PubMed=3120314;
RA Prioli R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
RA Pereira M.E.A.;
RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
RT neuraminidase, to high-density lipoprotein.";
RL Science 238:1417-1419(1987).
RN [18]
RP SEQUENCE OF 25-42.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [19]
RP PALMITOYLATION.
RX MEDLINE=86140194; PubMed=3005308;
RA Hoeg J.M., Meng M.S., Ronan R., Fairwell T., Brewer H.B. Jr.;
RT "Human apolipoprotein A-I. Post-translational modification by fatty
RT acid acylation.";
RL J. Biol. Chem. 261:3911-3914(1986).
RN [20]
RP PROCESSING.
RX MEDLINE=83195100; PubMed=6405383;
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
RA Breslow J.L.;
RT "Intracellular and extracellular processing of human apolipoprotein A-
RT I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
RN [21]
RP STRUCTURE BY NMR OF 190-209.
RX MEDLINE=96270776; PubMed=8664326;
RA Wang G., Treleaven W.D., Cushley R.J.;
RT "Conformation of human serum apolipoprotein A-I(166-185) in the
RT presence of sodium dodecyl sulfate or dodecylphosphocholine by 1H-NMR
RT and CD. Evidence for specific peptide-SDS interactions.";
RL Biochim. Biophys. Acta 1301:174-184(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.
RX MEDLINE=98024124; PubMed=9356442;
RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
RT "Crystal structure of truncated human apolipoprotein A-I suggests a
RT lipid-bound conformation.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
RN [23]
RP DISEASE.
RX MEDLINE=94059128; PubMed=8240372;
RA Nakata K., Kobayashi K., Yanagi H., Shimakura Y., Tsuchiya S.,
RA Arinami T., Hamaguchi H.;
RT "Autosomal dominant hypopalpalipoproteinemia due to a completely

RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis;
RX MEDLINE=92305062; PubMed=1610902;
RA Murray R.W., Marotti K.R.;
RT "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
RT and corresponding flanking regions.";
RL Biochim. Biophys. Acta 1131:207-210(1992).
RN [3]
RP SEQUENCE OF 25-48.
RC SPECIES=M.fascicularis;
RX MEDLINE=87185451; PubMed=3105581;
RA Herbert P.N., Bausserman L.L., Lynch K.M., Saritelli A.L.,
RA Kantor M.A., Nicolosi R.J., Shulman R.S.;
RT "Homologues of the human C and A apolipoproteins in the Macaca
RT fascicularis (cynomolgus) monkey.";
RL Biochemistry 26:1457-1463(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas; TISSUE=Liver;
RX MEDLINE=89232739; PubMed=2907746;
RA Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandeberg J.L.;
RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
RT clone and identification of DNA polymorphisms for genetic studies of
RT cholesterol metabolism.";
RL Gene 74:483-490(1988).
RN [5]
RP SEQUENCE OF 1-10 FROM N.A.
RC SPECIES=M.fascicularis;
RA Sorci-Thomas M.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
CC cholesterol acyltransferase (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M15411; AAA36834.1; -.
DR EMBL; M83242; AAA36832.1; -.
DR EMBL; M35634; AAA35380.1; -.
DR EMBL; M69223; AAA36831.1; -.
DR PIR; A26529; A26529.
DR HSSP; P02647; 1GW4.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Cholesterol metabolism; Direct protein sequencing; HDL;
KW Lipid transport; Plasma; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 267 Apolipoprotein A-I.
FT DOMAIN 68 267 10 X approximate tandem repeats.
FT REPEAT 68 89 1.
FT REPEAT 90 111 2.
FT REPEAT 112 122 3 (half-length).
FT REPEAT 123 144 4.
FT REPEAT 145 166 5.
FT REPEAT 167 188 6.
FT REPEAT 189 210 7.
FT REPEAT 211 232 8.
FT REPEAT 233 243 9 (half-length).
FT REPEAT 244 267 10.

FT CONFLICT 13 13 L -> P (in Ref. 1).
SQ SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;

Query Match 95.9%; Score 1306; DB 1; Length 267;
Best Local Similarity 95.1%; Pred. No. 5e-64;
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKAAVLTAVLFLTGSQARHFQODEPPQSPWDRVKOLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKATVLTAVLFLTGSQARHFQODEPPQTPWDRVKDLTVYVEALKDSGKDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTVSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEEEMELYRQVVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db 121 VQPYLDDFQKKWQEEEMELYRQVVEPLRAELHEGTRQKLHELHEKLSPLGEEVRDRARAHV 180

QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKASEHLSLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALEEYTKKLSTQ 267

RESULT 5
Q6LDN9 PRELIMINARY; PRT; 249 AA.
AC Q6LDN9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE APOA1 protein (Fragment).
GN Name=APOA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89377481; PubMed=2673706;
RA Moguilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Bollen A.;
RT "Production of human recombinant proapolipoprotein A-I in Escherichia
RT coli: purification and biochemical characterization.";
RL DNA 8:429-436(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Moguilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Bollen A.;
RL Submitted (APR-1990) to the EMBL/GenBank/DBSJ databases.
DR EMBL; M29068; AAA51747.1; -.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
FT NON_TER 1 1
FT CHAIN 7 249 Potential.
SQ SEQUENCE 249 AA; 28961 MW; C0A0B0B53903FAB4 CRC64;

Query Match 94.1%; Score 1281; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 RHFWQODEPPQSPWDRVKOLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVT 78
Db 1 RHFWQODEPPQSPWDRVKOLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVT 60

QY 79 STFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMEL 138

Db 61 STFSKLRQLGPVTQEFWDNLEKSTEGLRQEMSKDLSEVKAKVQPYLDLDFQKKWQEEML 120
QY 139 YRQKVEPLRAELQEGARQKHLHELQKLSPLGSEMRDRARAHVDALRTHLAPYSDELQRQL 198
Db 121 YRQKVEPLRAELQEGARQKHLHELQKLSPLGSEMRDRARAHVDALRTHLAPYSDELQRQL 180
QY 199 AARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALE 258
Db 181 AARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALE 240
QY 259 EYTKKLNTQ 267
Db 241 EYTKKLNTQ 249

RESULT 6
AAAS1747
ID AAAS1747 PRELIMINARY; PRT; 249 AA.
AC AAAS1747;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE APOA1 protein (Fragment).
GN APOA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Moguilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Bollen A.;
RT "Production of human recombinant proapolipoprotein A-I in Escherichia
RT coli: purification and biochemical characterization.";
RL DNA 8:429-436(1989).
DR EMBL; M29068; AAA51747.1; --
FT NON_TER 1 1
FT CHAIN 7 249 POTENTIAL.
SQ SEQUENCE 249 AA; 28961 MW; COA0B0B53903FAB4 CRC64;

Query Match 94.1%; Score 1281; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 RHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVT 78
Db 1 RHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVT 60
QY 79 STFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLSEVKAKVQPYLDLDFQKKWQEEML 138
Db 61 STFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLSEVKAKVQPYLDLDFQKKWQEEML 120
QY 139 YRQKVEPLRAELQEGARQKHLHELQKLSPLGSEMRDRARAHVDALRTHLAPYSDELQRQL 198
Db 121 YRQKVEPLRAELQEGARQKHLHELQKLSPLGSEMRDRARAHVDALRTHLAPYSDELQRQL 180
QY 199 AARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALE 258
Db 181 AARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALE 240
QY 259 EYTKKLNTQ 267
Db 241 EYTKKLNTQ 249

RESULT 7
APAI_CANFA
ID APA1 CANFA STANDARD; PRT; 266 AA.
AC P02648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN Name=APOA1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90132271; PubMed=2515239;
RA Luo C.-C., Li W.-H., Chan L.;
RT "Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs:
RT implications for the evolution and functional constraints of
RT apolipoprotein structure.";
RL J. Lipid Res. 30:1735-1746(1989).
RN [2]
RP SEQUENCE OF 25-266.
RX MEDLINE=82142425; PubMed=6801039;
RA Chung H., Randolph A., Reardon I., Heinrikson R.L.;
RT "The covalent structure of apolipoprotein A-I from canine high density
RT lipoproteins.";
RL J. Biol. Chem. 257:2961-2967(1982).
RN [3]
RP SEQUENCE OF 25-57 AND 262-265.
RX MEDLINE=76210910; PubMed=179887;
RA Nakai T., Whayne T.F., Tang J.;
RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein
RT A-i.";
RL FEBS Lett. 64:409-411(1976).
RN [4]
RP SEQUENCE OF 25-37.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
CC cholesterol acyltransferase (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons. Synthesized in the liver and small intestine.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
DR PIR; A60940; LPDGA1.
DR HSSP; P02647; IAVI.
DR HSC-2DPAGE; P02648; DOG.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Cholesterol metabolism; Direct protein sequencing; HDL;
KW Lipid transport; Plasma; Repeat; Signal.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 24
FT CHAIN 25 266 Apolipoprotein A-I.
FT DOMAIN 67 266 10 X approximate tandem repeats.
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (half-length).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 231 8.

FT REPEAT 232 242 9 (half-length).
FT REPEAT 243 266 10.
FT CONFLICT 168 168 A -> G (in Ref. 2).
FT CONFLICT 202 202 E -> Q (in Ref. 2).
FT CONFLICT 235 235 E -> Q (in Ref. 2).
FT CONFLICT 264 266 NAQ -> A (in Ref. 3).
SQ SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;

Query Match 85.3%; Score 1161.5; DB 1; Length 266;
Best Local Similarity 85.0%; Pred. No. 4e-56;
Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKAAVLT LAVFLTCGQARHFHQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKAALLT LAVFLTCGQARHFHQDE-PQSPWDRVKDLATVYVDAVKDSGRDYVAQFEAS 59

QY 61 ALGQNLKLLDNWDSVTSTFSKLREQLGPVTOEFWDNLEKETETGLRQEMSKDLEEVKAK 120
Db 60 ALGQNLKLLDNWDSLSSTVTKLREQIGPVTOEFWDNLEKETETEVLRQEMSKDLEEVKQK 119

QY 121 VQPYLDDFQKKQWEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGHEMRDRARHV 180
Db 120 VQPYLDDFQKKQWEEVELYRQKVAPLGSELREGARQKLOELOEKLSPLAELDRARTHV 179

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAEBYHAKATEHLSTLSBKAKPALEDLRQ 240
Db 180 DALRAQLAPYSDDLRLERLARLEALKEGGASLAEBYHARASEQLSALGKARPALEDLRQ 239

QY 241 GLLPVLESFKVSFLSALEEYTKKLNTO 267
Db 240 GLLPVLESFKVSLAALAAIDEATKKLNAQ 266

RESULT 8

APAL_PIG STANDARD; PRT; 265 AA.
ID APAL_PIG AC P18648;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN Name=APOA1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93224154; PubMed=8468059;
RA Birchbauer A., Knipping G., Juritsch B., Aschauer H., Zechner R.;
RT "Characterization of the apolipoprotein AI and CIII genes in the domestic pig."
RL Genomics 15:643-652(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Liver;
RX MEDLINE=94125128; PubMed=8294940;
RA Moeckel B., Zinke H., Flach R., Weiss B., Weiler-Guettler H.,
RA Gassen H.;
RT "Expression of apolipoprotein A-I in porcine brain endothelium in vitro."
RL J. Neurochem. 62:788-798(1994).
RN [3]
RP SEQUENCE OF 34-265 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90132667; PubMed=2105375;
RA Weiler-Guettler H., Sommerfeldt M., Papandrikopoulou A., Mischek U.,
RA Bonitz D., Frey A., Grupe M., Scheerer J., Gassen H.G.;
RT "Synthesis of apolipoprotein A-1 in pig brain microvascular endothelial cells."
RL J. Neurochem. 54:444-450(1990).
RN [4]
RP SEQUENCE OF 105-265 FROM N.A.

RC TISSUE=Liver;
RX MEDLINE=93154581; PubMed=8428656;
RA Trieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;
RT "Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs."
RL Gene 123:173-179(1993).
RN [5]
RP SEQUENCE OF 25-265.
RA Hasler-Rapacz J.O., Chaudhary R., Chowdhary B.P., Trieu V.N.,
RA Jackson K., Gustavsson I., Rapacz J.;
RL Submitted (OCT-1995) to Swiss-Prot.
RN [6]
RP SEQUENCE OF 25-34.
RX MEDLINE=76184721; PubMed=178359;
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus patas monkey."
RL Biochemistry 15:1928-1933(1976).
CC -!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in chylomicrons. Synthesized predominantly in the intestine and the liver.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC
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CC
CC EMBL; L00626; AAA30992.1; -.
CC EMBL; X69477; CAA49234.1; -.
CC EMBL; X17057; -; NOT ANNOTATED_CDS.
CC EMBL; X59414; CAA42050.1; -.
CC PIR; A46018; A46018.
CC PIR; JT0672; JT0672.
CC PIR; S21830; S21830.
CC PIR; S31394; S31394.
CC HSSP; P02647; 1AV1.
CC InterPro; IPR000074; Apolipoprotein.
CC InterPro; IPR009074; Apolipo_A_E_C3.
CC Pfam; PF01442; Apolipoprotein; 1.
KW Cholesterol metabolism; Direct protein sequencing; HDL;
KW Lipid transport; Plasma; Repeat; Signal.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 24
FT CHAIN 25 265 Apolipoprotein A-I.
FT DOMAIN 67 265 10 X approximate tandem repeats.
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (half-length).
FT REPEAT 122 142 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 230 8.
FT REPEAT 231 241 9 (half-length).
FT REPEAT 242 265 10.
FT CONFLICT 108 108 E -> K (in Ref. 3).
FT CONFLICT 143 143 Missing (in Ref. 2 and 3).
FT CONFLICT 173 173 D -> S (in Ref. 4).
FT CONFLICT 180 180 E -> A (in Ref. 2 and 3).
FT CONFLICT 185 186 HV -> QL (in Ref. 1 and 5).
FT CONFLICT 209 209 G -> D (in Ref. 2 and 3).
FT CONFLICT 224 224 A -> G (in Ref. 4).
SQ SEQUENCE 265 AA; 30325 MW; 2C6E578318ECF69C CRC64;

Query Match 81.1%; Score 1105; DB 1; Length 265;
Best Local Similarity 80.9%; Pred. No. 4.9e-53;
Matches 216; Conservative 20; Mismatches 29; Indels 2; Gaps 2;

QY 1 MKA AVLTLAVLFLTGSOARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKA AVLTLAVLFLTGSOARHFQQDD-PQSPWDRVKDFATVYVDAIKDSGRDYVAQFEAS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 60 ALGKHLNLKLLDNWDSLGSTFTKVRQGLGPVTQSFWDNLEKETETEARQEMSKDLEEVKKK 119

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db 120 VQPYLDDFQKKWQEMETYRQKMAPLGAEFREGARQKVQELQEKLSPLAEELRDLRAHV 179

QY 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 EALRQHVAPYSDDLQRMAARFEALKEGGGS-LAAYQAKAQEQLKALGEKAKPALEDLRQ 238

QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
Db 239 GLLPVLENLKVSIILAAIDEASKKLNAQ 265

RESULT 9
APAI_RABBIT STANDARD; PRT; 266 AA.

AC P09809;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN Name=APOA1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2ZAP AI; TISSUE=Small intestine;
RA Paraskevopoulou T.B., Kritis A., Zannis V.I.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=88082866; PubMed=3121329;
RA Pan T.C., Hao Q.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,
RA Kroon P.A., Chao Y.S.;
RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit
RT apolipoprotein A-I is synthesized in the intestine but not in the
RT liver.";
RL Eur. J. Biochem. 170:99-104(1987).
RN [3]
RP SEQUENCE OF 25-266.
RX MEDLINE=87030294; PubMed=3095115;
RA Yang C., Yang T., Pownall H.J., Gotto A.M. Jr.;
RT "The primary structure of apolipoprotein A-I from rabbit high-density
RT lipoprotein.";
RL Eur. J. Biochem. 160:427-431(1986).
CC -!- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
CC cholesterol acyltransferase (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

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CC -----

DR EMBL; X15908; CAA34024.1; -;
DR EMBL; X06658; CAA29857.1; -;
DR EMBL; X06659; CAA29858.1; -;
DR FIR; S06064; LPRB1Z.
DR HSSP; P02647; IAV1.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Cholesterol metabolism; Direct protein sequencing; HDL;
KW Lipid transport; Plasma; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 266 Apolipoprotein A-I.
FT DOMAIN 67 266 10 X approximate tandem repeats.
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (half-length).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 231 8.
FT REPEAT 232 242 9 (half-length).
FT REPEAT 243 266 10.
FT CONFLICT 18 18 A -> R (in Ref. 2; CAA29858).
FT CONFLICT 44 44 Missing (in Ref. 3).
FT CONFLICT 45 45 V -> I (in Ref. 2; CAA29858).
FT CONFLICT 107 107 E -> Q (in Ref. 3).
FT CONFLICT 123 123 Y -> F (in Ref. 2; CAA29857).
FT CONFLICT 147 147 A -> V (in Ref. 2; CAA29858 and 3).
FT CONFLICT 150 150 R -> G (in Ref. 2; CAA29858/CAA29857).
FT CONFLICT 191 191 N -> Q (in Ref. 3).
FT CONFLICT 195 195 Missing (in Ref. 2; CAA29858/CAA29857).
FT CONFLICT 211 211 S -> K (in Ref. 2; CAA29858/CAA29857).
FT CONFLICT 255 256 VL -> LV (in Ref. 3).
FT CONFLICT 256 256 L -> V (in Ref. 2; CAA29858/CAA29857).
SQ SEQUENCE 266 AA; 30591 MW; 0FF6DB386497C7D2 CRC64;

Query Match 80.8%; Score 1100.5; DB 1; Length 266;
Best Local Similarity 80.1%; Pred. No. 8.6e-53;
Matches 214; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

QY 1 MKA AVLTLAVLFLTGSOARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKA AVLTLAVLFLTGSOARHFQORDE-PRSSWDKIKDFATVYVDTVKDSGREYVAQFEAS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 60 AFGKQLNLKLLDNWDSLSSTVSKLQEQGLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 119

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db 120 VQPYLDDFQKKWQEVERYRQKVEPLGAELRESARQKLTELQEKLSPLAEELRDSARTHV 179

QY 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 DTLRTKLAPYSNELQORLAARLESIKEGGASLAAYQAKAREHL SVLSEKARPALEDLRQ 239

QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
Db 240 GLLPVLESFKASVQNVLDATKKLNTQ 266

RESULT 10
APAI_BOVIN
ID _APAI_BOVIN STANDARD; PRT; 265 AA.
AC P15497;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)

Q8HZ97 ID Q8HZ97 PRELIMINARY; PRT; 191 AA.
AC Q8HZ97;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA O'huigin C., Tichy H., Klein J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092007; AAM76624.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 1 1
FT NON_TER 191 191
SQ SEQUENCE 191 AA; 22087 MW; 2D30919874C8F0F4 CRC64;

Query Match 70.6%; Score 962; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2.3e-45;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 97
Db 1 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 60

QY 98 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQK 157
Db 61 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPXRAELQEGARQK 120

QY 158 LHELOEKLSPIDGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEALKENGGARLAEYH 217
Db 121 LHELOEKLSPIDGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEALKENGGARLAEYH 180

QY 218 AKATEHLSTLS 228
Db 181 AKATEHLSTLS 191

RESULT 15
Q8HZ95 ID Q8HZ95 PRELIMINARY; PRT; 191 AA.
AC Q8HZ95;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA O'huigin C., Tichy H., Klein J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092009; AAM76626.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.

KW Lipoprotein.
FT NON_TER 1 1
FT NON_TER 191 191
SQ SEQUENCE 191 AA; 22128 MW; D8D0671444C13725 CRC64;

Query Match 69.5%; Score 947; DB 2; Length 191;
Best Local Similarity 96.9%; Pred. No. 1.5e-44;
Matches 185; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 38 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 97
Db 1 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSMTSTFSKLREQLGPVTQEFWD 60

QY 98 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQK 157
Db 61 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPXRAELQEGARQK 120

QY 158 LHELOEKLSPIDGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEALKENGGARLAEYH 217
Db 121 LHELHEKLSPLGEEEXRDRARAHVDALRTHLAPYTDELQRQRLAARLEALKENGGARLAEYH 180

QY 218 AKATEHLSTLS 228
Db 181 AKASEHLSTLS 191

Search completed: December 21, 2004, 07:40:27
Job time : 159.462 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 06:24:01 ; Search time 159.744 Seconds
(without alignments)
599.590 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKA AVLTLAVLFLTG SQARH.....SPKVSFLSALEEYTKY LNTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|--------|-------|--------|----|----------|-------------|
| 1 | 1362 | 100.0 | 267 | 1 | AAP61079 | Assumed h |
| 2 | 1362 | 100.0 | 267 | 1 | AAP82128 | Entire hu |
| 3 | 1362 | 100.0 | 267 | 2 | AAR72705 | Human apo |
| 4 | 1362 | 100.0 | 267 | 2 | AAR34032 | Sequence |
| 5 | 1362 | 100.0 | 267 | 2 | AAY18675 | Human apo |
| 6 | 1362 | 100.0 | 267 | 4 | AAB47620 | Full leng |
| 7 | 1362 | 100.0 | 267 | 5 | AAO15892 | Human apo |
| 8 | 1362 | 100.0 | 267 | 5 | ABG97593 | Human apo |
| 9 | 1362 | 100.0 | 267 | 6 | ABR44031 | Human apo |
| 10 | 1362 | 100.0 | 267 | 6 | ABP57065 | Human apo |
| 11 | 1362 | 100.0 | 267 | 6 | ADA61214 | Human apo |
| 12 | 1362 | 100.0 | 267 | 7 | ADJ83084 | Human apo |
| 13 | 1362 | 100.0 | 267 | 8 | ADI19752 | Human APO |
| 14 | 1362 | 100.0 | 275 | 6 | AAO30162 | Human APO |
| 15 | 1359 | 99.8 | 267 | 7 | ADJ68447 | Human hea |
| 16 | 1359 | 99.8 | 267 | 7 | ADJ83083 | Human pro |
| 17 | 1355 | 99.5 | 267 | 6 | ABR44032 | Human mut |
| 18 | 1354 | 99.4 | 267 | 2 | AAW08602 | Human apo |
| 19 | 1351.5 | 99.2 | 268 | 1 | AAP80668 | Recombina |
| 20 | 1346 | 98.8 | 267 | 8 | ADE76862 | Human pro |
| 21 | 1328 | 97.5 | 299 | 4 | AAU33170 | Novel hum |
| 22 | 1306 | 95.9 | 267 | 7 | ADJ83086 | Apolipopr |
| 23 | 1299 | 95.4 | 267 | 7 | ADJ83087 | Crab-eati |
| 24 | 1281 | 94.1 | 249 | 7 | ADJ83085 | Human pro |
| 25 | 1276 | 93.7 | 250 | 5 | AAE24642 | Human Pro |

| | | | | | | |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 1268.5 | 93.1 | 252 | 6 | ABR43302 | Abr43302 Human lip |
| 27 | 1246.5 | 91.5 | 306 | 5 | ABG97587 | Abg97587 Human apo |
| 28 | 1246.5 | 91.5 | 325 | 5 | ABG97603 | Abg97603 Human apo |
| 29 | 1246 | 91.5 | 304 | 5 | ABG97586 | Abg97586 Human apo |
| 30 | 1246 | 91.5 | 304 | 5 | ABG97585 | Abg97585 Human apo |
| 31 | 1246 | 91.5 | 323 | 5 | ABG97602 | Abg97602 Human apo |
| 32 | 1246 | 91.5 | 323 | 5 | ABG97601 | Abg97601 Human apo |
| 33 | 1245 | 91.4 | 254 | 7 | ADD29962 | Add29962 Mature hu |
| 34 | 1243.5 | 91.3 | 304 | 5 | ABG97584 | Abg97584 Human apo |
| 35 | 1243.5 | 91.3 | 306 | 5 | ABG97588 | Abg97588 Human apo |
| 36 | 1243.5 | 91.3 | 306 | 5 | ABG97589 | Abg97589 Human apo |
| 37 | 1243.5 | 91.3 | 323 | 5 | ABG97600 | Abg97600 Human apo |
| 38 | 1243.5 | 91.3 | 325 | 5 | ABG97604 | Abg97604 Human apo |
| 39 | 1243.5 | 91.3 | 325 | 5 | ABG97605 | Abg97605 Human apo |
| 40 | 1242.5 | 91.2 | 337 | 5 | ABG97595 | Abg97595 Human apo |
| 41 | 1242 | 91.2 | 301 | 5 | ABG97583 | Abg97583 Human apo |
| 42 | 1242 | 91.2 | 301 | 5 | ABG97581 | Abg97581 Human apo |
| 43 | 1242 | 91.2 | 316 | 5 | ABG97599 | Abg97599 Human apo |
| 44 | 1242 | 91.2 | 316 | 5 | ABG97596 | Abg97596 Human apo |
| 45 | 1242 | 91.2 | 329 | 5 | ABG97592 | Abg97592 Human apo |

ALIGNMENTS

RESULT 1
AAP61079
ID AAP61079 standard; protein; 267 AA.
XX
AC AAP61079;
XX
DT 25-MAR-2003 (revised)
DT 07-OCT-1991 (first entry)
XX
DE Assumed human apolipoprotein A-1 derivative gene product.
XX
KW Hyperlipaemia; arteriosclerosis.
XX
OS Homo sapiens.
XX
PN JP61096998-A.
XX
PD 15-MAY-1986.
XX
PF 16-OCT-1984; 84JP-00216988.
XX
PR 16-OCT-1984; 84JP-00216988.
XX
(MITU) MITSUBISHI CHEM IND LTD.
XX
DR WPI; 1986-165025/26.
DR N-PSDB; AAN60886.
XX
PT Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA fragment in
PT cloning site downstream of expression vector promoter and introducing
PT into host microorganism.
XX
PS Disclosure; Fig 2; 9pp; Japanese.
XX
CC The human apolipoprotein may be produced by a suitable transformed host,
CC it is effective in treating hyperlipaemia and arteriosclerosis. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 3e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
|||||
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
|||||
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHLEQEKLSPLGEEMRDRARAHV 180
|||||
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHLEQEKLSPLGEEMRDRARAHV 180
|||||
QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
|||||
Db 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
|||||
QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
|||||
Db 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
|||||

RESULT 2
AAP82128
ID AAP82128 standard; protein; 267 AA.
XX
AC AAP82128;
XX
DT 25-MAR-2003 (revised)
DT 24-OCT-1990 (first entry)
XX
DE Entire human preproapoprotein A1.
XX
KW human preproapoprotein A1; high density lipoprotein deficiency; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .18
FT /label= precursor
FT Peptide 19. .24
FT /label= propeptide
FT Protein 25. .267
FT /label= mature apoprotein
XX
PN EP293357-A.
XX
PD 30-NOV-1988.
XX
PF 24-MAY-1988; 88EP-00870095.
XX
PR 28-MAY-1987; 87GB-00012540.
XX
PA (UNIO) UCB SA.
XX (BOLL/) BOLLEN A.
PI Bollen A, Gobert J, Wulfert E;
XX
DR WPI; 1988-339891/48.
DR N-PSDB; AAN82064.
XX
PT New DNA encoding human pro-apo-lipoprotein A1 - modified to eliminate
PT hairpin structures.
PS Disclosure; Page ?; 25pp; French.
XX
CC The cDNA 878bp fragment encoding preproapoprotein A1 was detected in
CC clone pULB1609 derived from human liver cells. See also AAN81258.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 3e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
|||||

Db 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
|||||
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
|||||
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHLEQEKLSPLGEEMRDRARAHV 180
|||||
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHLEQEKLSPLGEEMRDRARAHV 180
|||||
QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
|||||
Db 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
|||||
QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
|||||
Db 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
|||||

RESULT 3
AAR72705
ID AAR72705 standard; protein; 267 AA.
XX
AC AAR72705;
XX
DT 31-OCT-1995 (first entry)
XX
DE Human apo A-I including signal and propeptide sequences.
XX
KW Apo A-I; LDL cholesterol; low density lipoprotein; lipid.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .18
FT /label= presignal
FT Peptide 19. .240
FT /label= claimed
FT /note= "as part of fusion polypeptide"
FT Peptide 19. .24
FT /label= propeptide
FT Peptide 120. .135
FT /label= claimed
FT /note= "as part of fusion polypeptide"

XX US5408038-A.
XX
PD 18-APR-1995.
XX
PF 08-OCT-1992; 92US-00959946.
XX
PR 09-OCT-1991; 91US-00774633.
PR 18-JUN-1992; 92US-00901706.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Witztum JL, Koduri KR, Young SG, Smith RS, Curtiss LK;
XX
DR WPI; 1993-134378/16.
DR N-PSDB; AAQ89634.
XX
PT Polypeptide mimic of native apo B-100 and native apo A-I - useful in
PT assays for LDL and HDL in plasma samples.
XX
PS Claim 10; Fig 2; 41pp; English.

XX
CC AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its
CC corresp. cDNA, including presignal residues and propeptide residues,
CC according to Seilhamer et al., DNA 3(4):309 (1984). A dispersible apo A-
CC I/B-100 fusion polypeptide is claimed which contains a first AA sequence
CC of apo A-I and that includes at least AA sequence positions 120-135 (see
CC AAR72606) and which reacts with pan anti-apo AI antibodies such as: AI-4
CC ATCC HB8744; AI-7 ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI

analogue or variant, and X is heterologous group e.g., amino acid, peptide, protein, carbohydrate or a nucleic acid, providing that when (I) consists of exactly two identical, native apolipoproteins these are linked serially. (I) is useful for preparing a pharmaceutical composition which further comprises excipients, adjuvants, additives, such as phospholipids, cholesterol or triglycerides. (I) is useful or treating and/or preventing arteriosclerosis, for removing endotoxins, for treating angina pectoris including plaque or unstable angina pectoris, myocardial infarction, arterial stenoses such as claudicatio, carotis stenosis, cerebral arterial stenosis and other cardiovascular diseases. The nucleic acid (II) encoding (I) is useful for gene therapy, where the DNA sequence encoding (I) is used for transfection or infection of at least one cell population comprising macrophages or liver cells. (I) has a half-life of at least the half-life of native apoA-I, A-II or A-IV, preferably two times higher or more preferably 10 times higher than the half-life of the apoA molecules. (I) also has a higher binding affinity to cholesterol compared to native apoA-I, A-II or A-IV. (I) causes substantially no immune response in humans. This is the amino acid sequence of a human apolipoprotein (Apo) analogue fragment

Sequence 267 AA;

```
Query Match      100.0%; Score 1362; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. NO. 3e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

| | | | |
|----|-----|---|-----|
| QY | 1 | MKAAVLTLAVFLTGSQARHFQQDEPPQSPWDRVKOLATVYVDVLKDSGRDYVSQFEGS | 60 |
| Db | 1 | | 60 |
| QY | 61 | ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 |
| Db | 61 | | 120 |
| QY | 121 | VQPYLDDFQKKWQEEEMELYRKQVEPLRAELQEGAROKLHELQEKLSPLGEEMRDRARAHV | 180 |
| Db | 121 | | 180 |
| QY | 181 | DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ | 240 |
| Db | 181 | | 240 |
| QY | 241 | GLLPVLESFKVSFLSALEEYTKKLNTO | 267 |
| Db | 241 | | 267 |

| | |
|----------|--|
| RESULT 9 | |
| ABR44031 | |
| ID | ABR44031 standard; protein; 267 AA. |
| XX | |
| AC | ABR44031; |
| XX | |
| DT | 04-AUG-2003 (first entry) |
| XX | |
| DE | Human apolipoprotein A-I (ApoA-I) protein. |
| XX | |
| KW | Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; human; |
| KW | cardiovascular disorder. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| FT | Misc-difference 178 |
| FT | Location/Qualifiers |
| FT | /label= L178P |
| FT | /note= "wild-type Leu can be replaced with Pro" |

| | |
|----|-------------------------------|
| PN | WO2003035691-A1. |
| XX | |
| PD | 01-MAY-2003. |
| XX | |
| PF | 25-OCT-2002; 2002WO-CA001615. |
| XX | |

26-OCT-2001; 2001US-0335075P.
(XENO-) XENON GENETICS INC.
(UYBR-) UNIV BRITISH COLUMBIA.
Brownlie AJ, Dube M, Samuels M, Hayden MR;
WPI; 2003-449258/42.
N-PSDB; ACC48172.
New Apolipoprotein A-1 mutation, useful for preparing a composition for
treating cardiovascular disorder.
Claim 19; Page 33; 52pp; English.
The invention relates to a mutation of the apolipoprotein A-I (ApoA-I)
comprising a leucine to proline variant in position 178. The mutant ApoA-
I polynucleotide is useful for preparing a composition for treating
cardiovascular disorder. The present sequence represents a human ApoA-I
wild-type protein
Sequence 267 AA;

| Query Match | 100.0%; | Score 1362; | DB 6; | Length 267; |
|-----------------------|-----------------|---|-----------|-------------|
| Best Local Similarity | 100.0%; | Pred. NO. 3e-99; | | |
| Matches 267; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | MKAAVLTIAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS | 60 | |
| Db | 1 | MKAAVLTIAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS | 60 | |
| QY | 61 | ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 | |
| Db | 61 | ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 | |
| QY | 121 | VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV | 180 | |
| Db | 121 | VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV | 180 | |
| QY | 181 | DALRTHLAPYSDELQRQLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ | 240 | |
| Db | 181 | DALRTHLAPYSDELQRQLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ | 240 | |
| QY | 241 | GLLPVLESFKVSFLSALEYTKKLNTQ | 267 | |
| Db | 241 | GLLPVLESFKVSFLSALEYTKKLNTQ | 267 | |

RESULT 10
ABP57065
ID ABP57065 standard; protein; 267 AA.
XX
XX AC ABP57065;
XX
XX 14-APR-2003 (first entry)
XX
XX Human apolipoprotein (APOA1) protein SEQ ID NO:10.
XX
XX Atherosclerosis; pro-atherogenic inhibitor; antiatherosclerotic;
KW macrophage-specific expression element; gene therapy; apolipoprotein;
KW APOA1.
XX
XX Homo sapiens.
OS
XX
XX WO2003002061-A2.
PN
XX
XX 09-JAN-2003.
PD
XX
XX 26-JUN-2002; 2002WO-US020350.
PF
XX
XX 26-JUN-2001; 2001US-00893366.
PR
XX
XX (UYSA-) UNIV SAN DIEGO STATE FOUND.
PA

XX Davis RA;

PI WPI; 2003-201457/19.

XX N-PSDB; ABZ59334.

DR Novel nucleic acid useful for inhibiting or reducing atherosclerosis,

XX comprises nucleotide sequence encoding an inhibitor of a pro-atherogenic

PT molecule operationally linked to a macrophage-specific expression

PT element.

XX Disclosure; Page 95; 99pp; English.

XX The present invention describes a nucleic acid (I) comprising a

CC nucleotide sequence encoding an inhibitor of a pro-atherogenic molecule

CC operationally linked to a macrophage-specific expression element. Also

CC described: (1) a vector (II) comprising (I); (2) an embryonic stem cell

CC (III) comprising (I); (3) an isolated mammalian cell (IV) comprising (I);

CC (4) a recombinant cell (V) comprising a macrophage expressing nucleic

CC acid encoding an inhibitor of a pro-atherogenic molecule; (5) a

CC transgenic non-human mammal (VI) comprising recombinant cells containing

CC a transgenic nucleic acid encoding an inhibitor of a pro-atherogenic

CC molecule; and (6) a non-human mammalian cell (VII) isolated from (VI).

CC (I) has antiatherosclerotic activity and can be used in gene therapy. (I)

CC or (V) can be used for inhibiting or reducing atherosclerosis, by

CC administering to an individual (I) or a population of (V), where the

CC population of (V) is derived from leukocytes, monocytes, macrophages or

CC stem cells. (V) or (VI) is useful to screen for a drug potentially

CC effective for treating atherosclerosis. (V) is useful for identifying a

CC compound that reduces susceptibility to developing atherosclerosis. (VI)

CC is useful for determining the role of an inhibitor of pro-atherogenic

CC molecule in a particular pathological phenotype or condition of an animal

CC model for atherosclerosis used in drug development. The present sequence

CC represents human apolipoprotein (APOA1), which is given in the

XX exemplification of the present invention

SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 6; Length 267;

Best Local Similarity 100.0%; Pred. No. 3e-99;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVLFTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYSQFEGS 60

Db |||||||

QY 1 MKA AVLTLAVLFTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYSQFEGS 60

Db |||||||

QY 61 ALGQNLNKLNDWDSVTSTFSKLREQLGPVTQSFWDNLEKETEGRLQEMSKDLEEVKAK 120

Db |||||||

QY 61 ALGQNLNKLNDWDSVTSTFSKLREQLGPVTQSFWDNLEKETEGRLQEMSKDLEEVKAK 120

Db |||||||

QY 121 VQPYLDDFQKKQWEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHV 180

Db |||||||

QY 121 VQPYLDDFQKKQWEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHV 180

Db |||||||

QY 181 DALRTHLAPYSDELQRQLAARLEALKENGGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Db |||||||

QY 181 DALRTHLAPYSDELQRQLAARLEALKENGGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Db |||||||

QY 241 GLLPVLESFKVSFLSALSEYTKLNTQ 267

Db |||||||

QY 241 GLLPVLESFKVSFLSALSEYTKLNTQ 267

Db |||||||

RESULT 11

ADA61214

ID ADA61214 standard; protein; 267 AA.

XX AC ADA61214;

XX 20-NOV-2003 (first entry)

DT Human apolipoprotein A-1 (apo-A-1).

XX

KW Human; apolipoprotein A-I; apo-A-I; T-cell activation inhibitor-like;

KW AFTI; T-cell-mediated activation; monocyte; interleukin-beta; IL-1beta;

KW tumour necrosis factor alpha; TNF-alpha; gene therapy;

KW IL-1-mediated disease; acute pancreatitis; Alzheimer's disease; asthma;

KW cancer; diabetes; glomerulonephritis; multiple sclerosis; osteoporosis;

KW pain; Parkinson's disease; psoriasis; uveitis; TNF-mediated disease;

KW depression; pancreatitis; periodontal disease; pulmonary fibrosis;

KW reperfusion injury; rheumatic disease; septic shock;

KW systemic lupus erythematosus; thyroiditis; nontropic; neuroprotective;

KW cytostatic; nephrotropic; analgesic; ophthalmological; antiinflammatory;

KW vasotropic; antibacterial; immunosuppressive; dermatological.

XX Homo sapiens.

OS US2002064820-A1.

XX 30-MAY-2002.

XX 13-MAR-2001; 2001US-00803918.

PR 13-MAR-2000; 2000US-0189008P.

PR 31-MAR-2000; 2000US-0193551P.

XX (DAYE/) DAYER J.

PA (BURG/) BURGER D.

PA (KOHN/) KOHNO T.

PA (EDWA/) EDWARDS C K.

XX Dayer J, Burger D, Kohno T, Edwards CK;

PI WPI; 2003-615701/58.

XX N-PSDB; ADA61213.

DR New apolipoprotein A-I polypeptide or its related polypeptide termed apo-

PT A-I fragment T-cell activation inhibitor-like polypeptide, useful for

PT treating interleukin-1 or tumor necrosis factor-alpha mediated disease.

XX Claim 1; Fig 1A; 56pp; English.

PS The invention discloses a apolipoprotein A-I (apo-A-I) polypeptide or its

XX related polypeptide, apo-A-I fragment T-cell activation inhibitor-like

CC (AFTI) polypeptide, or a fragment or an allelic or splice variant. Apo-A-

CC I and its derivatives are used in regulating T-cell-mediated activation

CC of monocytes. Also disclosed is an antibody produced by immunising an

CC animal with apo-A-I and a selective binding agent, or its fragment. Apo-A

CC -I is useful for reducing inflammation, interleukin (IL)-beta secretion

CC or tumour necrosis factor (TNF)-alpha secretion in a subject, or for

CC treating IL-1 or TNF-alpha mediated disease in a subject. The

CC compositions of the invention are useful for treating (e.g. gene

CC therapy), preventing or ameliorating a medical condition involving

CC monocyte activation in a patient, for determining whether a compound

CC inhibits activity or production of apo-A-I, for detecting or quantifying

CC the amount of apo-A-I in a sample, for regulating T-cell-mediated

CC activation of monocytes, to identify a molecule that binds to apo-A-I,

CC for identifying AFTI receptors, for cloning AFTI receptors, and as an

CC immunogen to raise antibodies, for treating acute and chronic IL-1-

CC mediated diseases such as acute pancreatitis, Alzheimer's disease,

CC asthma, cancer, diabetes, glomerulonephritis, multiple sclerosis,

CC osteoporosis, pain, Parkinson's disease, psoriasis, uveitis, and acute

CC and chronic TNF-mediated diseases such as depression, pancreatitis,

CC periodontal diseases, pulmonary fibrosis, reperfusion injury, rheumatic

CC diseases, septic shock, systemic lupus erythematosus and thyroiditis.

CC They are also useful for regulating expression and modulating levels of

CC apo-A-I, as hybridisation probes in diagnostic assays, for diagnostic

CC applications, to test for the presence of apo-A-I in cells, for in vivo

CC imaging and in therapeutics. The sequence presented is the human apo-A-1

CC protein which comprises an 18K N-terminal or 13K N- or C-terminal

CC fragments of the apo-A-1 protein.

XX SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 6; Length 267;

Best Local Similarity 100.0%; Pred. No. 3e-99;

| | | | | | | |
|---|--------|--|---------------|-------------|----------------------|--|
| QY | 181 | DALRTHLAPYSDELQR | LAARLEALKENG | GARLAEYHAKA | TEHLSTLSEKAKPALEDLRQ | 240 |
| | | | | | | |
| Db | 181 | DALRTHLAPYSDELQR | LAARLEALKENG | GARLAEYHAKA | TEHLSTLSEKAKPALEDLRQ | 240 |
| | | | | | | |
| QY | 241 | GLLPVLESFKVSFLS | ALEEYTKKLN | TQ | 267 | |
| | | | | | | |
| Db | 241 | GLLPVLESFKVSFLS | ALEEYTKKLN | TQ | 267 | |
| | | | | | | |
| RESULT 13 | | | | | | |
| AD | 119752 | ADI19752 standard; protein; 267 AA. | | | | |
| ID | AD | 119752 | | | | |
| XX | AC | AD | 119752; | | | |
| XX | DT | 22-APR-2004 | (first entry) | | | |
| XX | DE | Human APOA1 | protein. | | | |
| XX | XX | Pro-atherogenic; atherosclerosis; therapy; human; apolipoprotein; APOA1; | | | | |
| KW | KW | macrophage-specific expression element. | | | | |
| XX | OS | Homo sapiens. | | | | |
| XX | PN | US2004001810-A1. | | | | |
| XX | PD | 01-JAN-2004. | | | | |
| XX | PF | 26-JUN-2002; 2002US-00186288. | | | | |
| XX | PR | 26-JUN-2002; 2002US-00186288. | | | | |
| XX | PA | (DAVI/) DAVIS R A. | | | | |
| XX | PI | Davis RA; | | | | |
| XX | DR | WPI; 2004-061641/06. | | | | |
| DR | DR | N-PSDB; ADI19751. | | | | |
| DR | DR | GENBANK; XM_006435. | | | | |
| XX | PT | New nucleic acids encoding an inhibitor of a pro-atherogenic molecule | | | | |
| PT | PT | operationally linked to a macrophage-specific expression element, useful | | | | |
| PT | PT | for reducing or inhibiting atherosclerosis. | | | | |
| XX | PS | Disclosure; SEQ ID NO 10; 45pp; English. | | | | |
| XX | CC | The present invention provides a nucleic acid comprising a nucleotide | | | | |
| CC | CC | sequence encoding an inhibitor of a pro-atherogenic molecule | | | | |
| CC | CC | operationally linked to a macrophage-specific expression element. The | | | | |
| CC | CC | invention is useful for reducing and inhibiting atherosclerosis. The | | | | |
| CC | CC | present sequence is human apolipoprotein (APOA1) protein. | | | | |
| XX | SQ | Sequence 267 AA; | | | | |
| Query Match 100.0%; Score 1362; DB 8; Length 267; | | | | | | |
| Best Local Similarity 100.0%; Pred. No. 3e-99; | | | | | | |
| Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0 | | | | | | |
| QY | 1 | MKAAVLT | LAVLFLTGS | QARHF | WQDEPPQSP | WDRVKDLATVYVDVLKDSGRDVSQFEGS 60 |
| | | | | | | |
| Db | 1 | MKAAVLT | LAVLFLTGS | QARHF | WQDEPPQSP | WDRVKDLATVYVDVLKDSGRDVSQFEGS 60 |
| | | | | | | |
| QY | 61 | ALGKQLNLKLLDN | WDSVTSTF | SKLREQL | GPVTQEF | WDNLEKETETGLRQEMSKDLEEVKAK 120 |
| | | | | | | |
| Db | 61 | ALGKQLNLKLLDN | WDSVTSTF | SKLREQL | GPVTQEF | WDNLEKETETGLRQEMSKDLEEVKAK 120 |
| | | | | | | |
| QY | 121 | VQPYLDD | FQKKWQ | EEMEL | YRKVEPL | RAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180 |
| | | | | | | |
| Db | 121 | VQPYLDD | FQKKWQ | EEMEL | YRKVEPL | RAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180 |
| | | | | | | |
| QY | 181 | DALRTHLAPYSDELQR | LAARLEALKENG | GARLAEYHAKA | TEHLSTLSEKAKPALEDLRQ | 240 |
| | | | | | | |

Db 181 DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 241

QY 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
 |||||

Db 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
 |||||

RESULT 14
 AAO30162
 ID AAO30162 standard; protein; 275 AA.
 XX AC AAO30162;
 AC AC
 XX DT 03-SEP-2003 (first entry)
 XX DE Human APOA1 protein.
 XX DE
 XX KW Human; aging-associated disease; oxidative stress; AAD; APOA1.
 XX OS Homo sapiens.
 XX PN WO2003045988-A2.
 XX PD 05-JUN-2003.
 XX PF 28-NOV-2002; 2002WO-EP013549.
 XX PR 29-NOV-2001; 2001EP-00204600.
 XX PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX PI Contreras RH, Chen C;
 XX PI WPI; 2003-505183/47.
 DR N-PSDB; AAL60806.
 DR
 XX
 PT Screening genes involved in aging and/or aging-associated diseases or in
 PT oxidative stress by mutating and cultivating a yeast cell, enriching the
 PT population, labeling the mother cells and isolating the highly labeled
 PT cells.
 XX
 PS Claim 13; Page 40; 78pp; English.
 XX
 CC The invention relates to a method for screening genes involved in aging
 CC and/or aging-associated diseases (AAD) or in oxidative stress. The method
 CC involves mutating and cultivating a yeast cell, enriching the population
 CC for mother cells, labelling the mother cells and isolating the highly
 CC labelled cells. The present sequence is human APOA1 protein. This
 CC sequence is used to illustrate the method of the invention
 XX
 SQ Sequence 275 AA;
 Query Match 100.0%; Score 1362; DB 6; Length 275;
 Best Local Similarity 100.0%; Pred. No. 3.2e-99;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MKA AVLTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDVSQFEGS 60
 |||||

Db 9 MKA AVLTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDVSQFEGS 68
 |||||

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
 |||||

Db 69 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 128
 |||||

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV 180
 |||||

Db 129 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV 188
 |||||

QY 181 DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
 |||||

Db 189 DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 248
 |||||

QY 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
 |||||

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OM protein - protein search, using sw model

Run on: December 21, 2004, 06:52:14 ; Search time 132.033 Seconds
(without alignments)
723.622 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKA AVLTLAVLFLTGSQARH.....SPKVSFLSALEYTKKLNTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1362 | 100.0 | 267 | 9 | US-09-803-918A-2 |
| 2 | 1362 | 100.0 | 267 | 9 | US-09-987-107-15 |
| 3 | 1362 | 100.0 | 267 | 10 | US-09-802-640-30 |
| 4 | 1362 | 100.0 | 267 | 14 | US-10-032-189-75 |
| 5 | 1362 | 100.0 | 267 | 14 | US-10-283-599-260 |
| 6 | 1362 | 100.0 | 267 | 14 | US-10-403-902A-30 |
| 7 | 1362 | 100.0 | 267 | 15 | US-10-186-288-10 |
| 8 | 1362 | 100.0 | 267 | 15 | US-10-038-854-219 |
| 9 | 1362 | 100.0 | 267 | 15 | US-10-038-854-226 |
| 10 | 1359 | 99.8 | 267 | 14 | US-10-032-189-74 |
| 11 | 1359 | 99.8 | 267 | 16 | US-10-408-765A-253 |
| 12 | 1346 | 98.8 | 267 | 10 | US-09-919-039-27 |
| 13 | 1306 | 95.9 | 267 | 9 | US-09-987-107-16 |

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| 14 | 1306 | 95.9 | 267 | 14 | US-10-032-189-77 | Sequence 77, Appl |
| 15 | 1306 | 95.9 | 267 | 15 | US-10-038-854-223 | Sequence 223, App |
| 16 | 1306 | 95.9 | 267 | 15 | US-10-038-854-230 | Sequence 230, App |
| 17 | 1299 | 95.4 | 267 | 14 | US-10-032-189-78 | Sequence 78, Appl |
| 18 | 1281 | 94.1 | 249 | 14 | US-10-032-189-76 | Sequence 76, Appl |
| 19 | 1281 | 94.1 | 249 | 15 | US-10-038-854-220 | Sequence 220, App |
| 20 | 1281 | 94.1 | 249 | 15 | US-10-038-854-227 | Sequence 227, App |
| 21 | 1276 | 93.7 | 250 | 15 | US-10-465-789A-2 | Sequence 2, Appli |
| 22 | 1246.5 | 91.5 | 306 | 9 | US-09-987-107-9 | Sequence 9, Appli |
| 23 | 1246 | 91.5 | 304 | 9 | US-09-987-107-7 | Sequence 7, Appli |
| 24 | 1246 | 91.5 | 304 | 9 | US-09-987-107-8 | Sequence 8, Appli |
| 25 | 1246 | 91.5 | 323 | 9 | US-09-987-107-58 | Sequence 58, Appl |
| 26 | 1246 | 91.5 | 323 | 9 | US-09-987-107-60 | Sequence 60, Appl |
| 27 | 1243.5 | 91.3 | 304 | 9 | US-09-987-107-6 | Sequence 6, Appli |
| 28 | 1243.5 | 91.3 | 306 | 9 | US-09-987-107-10 | Sequence 10, Appl |
| 29 | 1243.5 | 91.3 | 306 | 9 | US-09-987-107-11 | Sequence 11, Appl |
| 30 | 1243.5 | 91.3 | 323 | 9 | US-09-987-107-56 | Sequence 56, Appl |
| 31 | 1242.5 | 91.2 | 337 | 9 | US-09-987-107-46 | Sequence 46, Appl |
| 32 | 1242 | 91.2 | 301 | 9 | US-09-987-107-3 | Sequence 3, Appli |
| 33 | 1242 | 91.2 | 301 | 9 | US-09-987-107-5 | Sequence 5, Appli |
| 34 | 1242 | 91.2 | 316 | 9 | US-09-987-107-48 | Sequence 48, Appl |
| 35 | 1242 | 91.2 | 316 | 9 | US-09-987-107-54 | Sequence 54, Appl |
| 36 | 1242 | 91.2 | 329 | 9 | US-09-987-107-14 | Sequence 14, Appl |
| 37 | 1242 | 91.2 | 344 | 9 | US-09-987-107-68 | Sequence 68, Appl |
| 38 | 1241 | 91.1 | 243 | 9 | US-09-987-107-1 | Sequence 1, Appli |
| 39 | 1241 | 91.1 | 243 | 15 | US-10-038-854-221 | Sequence 221, App |
| 40 | 1241 | 91.1 | 243 | 15 | US-10-038-854-228 | Sequence 228, App |
| 41 | 1241 | 91.1 | 244 | 9 | US-09-987-107-2 | Sequence 2, Appli |
| 42 | 1241 | 91.1 | 261 | 9 | US-09-987-107-52 | Sequence 52, Appl |
| 43 | 1241 | 91.1 | 336 | 9 | US-09-987-107-44 | Sequence 44, Appl |
| 44 | 1238 | 90.9 | 324 | 9 | US-09-987-107-62 | Sequence 62, Appl |
| 45 | 1235 | 90.7 | 324 | 9 | US-09-987-107-64 | Sequence 64, Appl |

ALIGNMENTS

RESULT 1
US-09-803-918A-2
; Sequence 2, Application US/09803918A
; Patent No. US20020064820A1
; GENERAL INFORMATION:
; APPLICANT: Dayer, Jean-Michel
; APPLICANT: Burger, Danielle
; APPLICANT: Kohno, Tadahiko
; APPLICANT: Edwards III, Carl K.
; TITLE OF INVENTION: APO-A-1 REGULATION OF T-CELL SIGNALING
; FILE REFERENCE: 06843.0035-00000
; CURRENT APPLICATION NUMBER: US/09/803,918A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/189,008
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/193,551
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-803-918A-2

Query Match 100.0%; Score 1362; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1 | MKA AVLTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS | 60 |
| | | | |
| QY | 61 | ALGKQLNLKLDNWDSVTSTFSLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 |
| | | | |
| Db | 61 | ALGKQLNLKLDNWDSVTSTFSLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 |
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; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-189-75

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Query Match          100.0%; Score 1362; DB 14; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Dd | 1 | MKAAVLT | LAVLFLT | GSQARHFWQDEPPQSPWDRVKOLATVYVDVLKDSGRDVSQFEGS | 60 |
| Qy | 61 | ALGKQLNLKL | LDNWDSVTSTFSKLREQLGVPVTOEFWDNLEKETETGLRQEMSKDLSEEVKAK | 120 | |
| Dd | 61 | ALGKQLNLKL | LDNWDSVTSTFSKLREQLGVPVTOEFWDNLEKETETGLRQEMSKDLSEEVKAK | 120 | |
| Qy | 121 | VQPYLDDFQKKWQEEMELYRKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRAHV | 180 | | |
| Dd | 121 | VQPYLDDFQKKWQEEMELYRKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRAHV | 180 | | |
| Qy | 181 | DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ | 240 | | |
| Dd | 181 | DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ | 240 | | |
| Qy | 241 | GLLPVLESFKVSFLSALEEYTKKLNTQ | 267 | | |
| Dd | 241 | GLLPVLESFKVSFLSALEEYTKKLNTQ | 267 | | |

RESULT 5
US-10-283-599-260
; Sequence 260, Application US/10283599
; Publication No. US20030208059A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas

```

; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-283-599-260

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| Query Match | 100.0%; | Score 1362; | DB 14; | Length 267; |
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| Matches 267; Conservative | 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | MKAAVLTLAVLFLTGSQLRHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS | 60 | |
| Db | 1 | MKAAVLTLAVLFLTGSQLRHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS | 60 | |
| Qy | 61 | ALGKQLNLKLLDNWDSVTSTFPSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 | |
| Db | 61 | ALGKQLNLKLLDNWDSVTSTFPSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK | 120 | |
| Qy | 121 | VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV | 180 | |
| Db | 121 | VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV | 180 | |
| Qy | 181 | DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ | 240 | |
| Db | 181 | DALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ | 240 | |
| Qy | 241 | GLLPVLESFKVSFLSALEYTKKLNTQ | 267 | |
| Db | 241 | GLLPVLESFKVSFLSALEYTKKLNTQ | 267 | |

RESULT 6
US-10-403-902A-30
; Sequence 30, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna
; APPLICANT: Kley, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; CURRENT FILING DATE: 2003-07-21
; PRIORITY APPLICATION NUMBER: 09/802,640

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; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-403-902A-30

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Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MKAAVLT LAVLFTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
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QY      61 ALGQNLNKL LDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
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Db      61 ALGQNLNKL LDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
      |||||||

QY      121 VQPYLDDFQKKWQEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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Db      121 VQPYLDDFQKKWQEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
      |||||||

QY      181 DALRTHLAPYSDELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
      |||||||
Db      181 DALRTHLAPYSDELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
      |||||||

QY      241 GLLPVLESFKVSFLSALEYTKKLNQ 267
      |||||||
Db      241 GLLPVLESFKVSFLSALEYTKKLNQ 267
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RESULT 7
US-10-186-288-10
; Sequence 10, Application US/10186288
; Publication No. US20040001810A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger A.
; TITLE OF INVENTION: Compositions and Methods for Treating
; FILE REFERENCE: P-RD 5299
; CURRENT APPLICATION NUMBER: US/10/186,288
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 09/893,366
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-288-10

Query Match      100.0%; Score 1362; DB 15; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||||||
Db      1 MKAAVLT LAVLFTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
      |||||||

QY      61 ALGQNLNKL LDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
      |||||||
Db      61 ALGQNLNKL LDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
      |||||||

QY      121 VQPYLDDFQKKWQEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
      |||||||
Db      121 VQPYLDDFQKKWQEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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QY      181 DALRTHLAPYSDELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
      |||||||
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Db      181 DALRTHLAPYSDELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
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QY      241 GLLPVLESFKVSFLSALEYTKKLNQ 267
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Db      241 GLLPVLESFKVSFLSALEYTKKLNQ 267
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RESULT 8
US-10-038-854-219
; Sequence 219, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine B
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennnda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 219
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-219

Query Match      100.0%; Score 1362; DB 15; Length 267;
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[illegible]

RESULT 9

US-10-038-854-226
; Sequence 226, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimiro Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863

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; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 226
; LENGTH: 267
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-038-854-226

Query Match      100.0%; Score 1362; DB 15; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKAAVLTAVLFLTGSAARHFQQDEPPQSPWDRVKOLATVYDVVLKDSGRDYVSQFEGS 60
Db      1  MKAAVLTAVLFLTGSAARHFQQDEPPQSPWDRVKOLATVYDVVLKDSGRDYVSQFEGS 60

Qy     61  ALGQQLNLKLLDNWDSVTSTFSKLREQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db     61  ALGQQLNLKLLDNWDSVTSTFSKLREQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Qy    121  VQPYLDDFQKKWQEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHV 180
Db    121  VQPYLDDFQKKWQEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHV 180

Qy    181  DALRTHLAPYSDELQRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db    181  DALRTHLAPYSDELQRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy    241  GLLPVLESFKVSFLSALEYTKKLNTQ 267
Db    241  GLLPVLESFKVSFLSALEYTKKLNTQ 267

```

RESULT 10
US-10-032-189-74
; Sequence 74, Application US/10032189
; Publication No. US20030170630A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Grosse, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Gorman, Linda
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Rieger, Daniel K
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-228
; CURRENT APPLICATION NUMBER: US/10/032,189
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-189-74

Query Match 99.8%; Score 1359; DB 14; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.9e-92;
Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAVLTlAVLFLtGsqARHFwQDPPQSPwDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
|
Db 1 MKAAVLTlAVLFLtGsqARHFwQDPPQSPwDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTfSKLREQLGPVTQEFWDNLEKETEGlRQEMSKDLEEVKAK 120
|
Db 61 ALGKQLNLKLLDNWDSVTSTfSKLREQLGPVTQEFWDNLEKETEGlRQEMSKDLEEVKAK 120

QY 121 VQPYLDDfQKKWQEEmELyRQKVEPlRAELQEGARQKLHElQEKLSPlGEEMRDRAHv 180
|
Db 121 VQPYLDDfQKKWQEEmELyRQKVEPlRAELQEGARQKLHElQEKLSPlGEEMRDRAHv 180

QY 181 DALRTHLAPYSDELrQRLAARLEAlKENGgARLAeYHAKATeHlSTlSEKAKPALEDLRQ 240
|
Db 181 DALRTHLAPYSDELrQRLAARLEAlKENGgARLAeYHAKATeHlSTlSEKAKPALEDLRQ 240

QY 241 GLLPVLESfKVSfLSAlEeYTKKLNTQ 267
|
Db 241 GLLPVLESfKVSfLSAlEeYTKKLNTQ 267

RESULT 11
US-10-408-765A-253
; Sequence 253, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-253

Query Match 99.8%; Score 1359; DB 16; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.9e-92;
Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAVLTlAVLFLtGsqARHFwQDPPQSPwDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
|
Db 1 MKAAVLTlAVLFLtGsqARHFwQDPPQSPwDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTfSKLREQLGPVTQEFWDNLEKETEGlRQEMSKDLEEVKAK 120
|
Db 61 ALGKQLNLKLLDNWDSVTSTfSKLREQLGPVTQEFWDNLEKETEGlRQEMSKDLEEVKAK 120

QY 121 VQPYLDDfQKKWQEEmELyRQKVEPlRAELQEGARQKLHElQEKLSPlGEEMRDRAHv 180
|
Db 121 VQPYLDDfQKKWQEEmELyRQKVEPlRAELQEGARQKLHElQEKLSPlGEEMRDRAHv 180

QY 181 DALRTHLAPYSDELrQRLAARLEAlKENGgARLAeYHAKATeHlSTlSEKAKPALEDLRQ 240
|
Db 181 DALRTHLAPYSDELrQRLAARLEAlKENGgARLAeYHAKATeHlSTlSEKAKPALEDLRQ 240

QY 241 GLLPVLESfKVSfLSAlEeYTKKLNTQ 267
|
Db 241 GLLPVLESfKVSfLSAlEeYTKKLNTQ 267

RESULT 12
US-09-919-039-27
; Sequence 27, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 27
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 2516070CD1
US-09-919-039-27

Query Match 98.8%; Score 1346; DB 10; Length 267;
Best Local Similarity 98.9%; Pred. No. 1.8e-91;
Matches 264; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKAAVLTlAVLFLtGsqARHFwQDPPQSPwDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
|
Db 1 MKAAVLTlAVLFLtGsqARHFwQDPPQSPwDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTfSKLREQLGPVTQEFWDNLEKETEGlRQEMSKDLEEVKAK 120
|
Db 61 ALGKQLNLKLLDNWDSVTSTfSKLREQLGPVTQEFWDNLEKETEGlRQEMSKDLEEVKAK 120

QY 121 VQPYLDDfQKKWQEEmELyRQKVEPlRAELQEGARQKLHElQEKLSPlGEEMRDRAHv 180
|

Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLHELQEKLSPLGEMRDRARAHV 180
QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEBYHAKATEHLSLTLSEKAKPALEDLRQ 240
:|||||
Db 181 ARVRTHLAPYSDELQRRLAARLEALKENGARLAEBYHAKATEHLSLTLSEKAKPALEDLRQ 240
QY 241 GLLPVLESFKVSFLSALBEYTKKLNTQ 267
|||||
Db 241 GLLPVLESFKVSFLSALBEYTKKLNTQ 267

RESULT 13
US-09-987-107-16
; Sequence 16, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-987-107-16

Query Match 95.9%; Score 1306; DB 9; Length 267;
Best Local Similarity 95.1%; Pred. No. 1.6e-88;
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKAAVLT LAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
|||
Db 1 MKATVLT LAVLFTG SQARHFQQDEPPQTPWDRVKDLVTYVVEALKDSGKDYVSQFEGS 60
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
|||
Db 61 ALGKQLNLKLLDNWDSVTSTVSKLREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLHELQEKLSPLGEMRDRARAHV 180
|||||
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELHEGTRQKHLHELKLSPLGEEVRDRARAHV 180
QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEBYHAKATEHLSLTLSEKAKPALEDLRQ 240
|||||
Db 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEBYHAKASEHLSLTLSEKAKPALEDLRQ 240
QY 241 GLLPVLESFKVSFLSALBEYTKKLNTQ 267
|||||
Db 241 GLLPVLESFKVSFLSALBEYTKKLSTQ 267

RESULT 14
US-10-032-189-77
; Sequence 77, Application US/10032189
; Publication No. US20030170630A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M

; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Grosse, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Gorman, Linda
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Rieger, Daniel K
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-228
; CURRENT APPLICATION NUMBER: US/10/032,189
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-032-189-77

Query Match 95.9%; Score 1306; DB 14; Length 267;
Best Local Similarity 95.1%; Pred. No. 1.6e-88;
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKAAVLT LAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
|||
Db 1 MKATVLT LAVLFTG SQARHFQQDEPPQTPWDRVKDLVTYVVEALKDSGKDYVSQFEGS 60
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
|||||
Db 61 ALGKQLNLKLLDNWDSVTSTVSKLREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLHELQEKLSPLGEMRDRARAHV 180
|||||
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELHEGTRQKHLHELKLSPLGEEVRDRARAHV 180
QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEBYHAKATEHLSLTLSEKAKPALEDLRQ 240
|||||
Db 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEBYHAKASEHLSLTLSEKAKPALEDLRQ 240

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 10:45:04 ; Search time 16 Seconds
(without alignments)
1022.303 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_194
Perfect score: 885
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....RARAHVDALRTHLAPYSDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 85142

Minimum DB seq length: 0
Maximum DB seq length: 170

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | | |
|------------|-------|---------------|--------|----------|--------------------|--|
| Result No. | Score | Query Match % | Length | DB ID | Description | |
| 1 | 370 | 41.8 | 164 | 2 S21830 | apolipoprotein A-I | |
| 2 | 106 | 12.0 | 34 | 2 S67972 | apolipoprotein AI | |
| 3 | 106 | 12.0 | 36 | 2 A56866 | apolipoprotein A-I | |
| 4 | 101 | 11.4 | 20 | 2 A05313 | apolipoprotein A-I | |
| 5 | 98 | 11.1 | 118 | 2 B69818 | conserved hypothet | |
| 6 | 90.5 | 10.2 | 164 | 2 T23249 | hypothetical prote | |
| 7 | 90 | 10.2 | 146 | 2 G90201 | conserved hypothet | |
| 8 | 88 | 9.9 | 129 | 2 C95164 | conserved hypothet | |
| 9 | 88 | 9.9 | 129 | 2 B98030 | ski-related protei | |
| 10 | 86.5 | 9.8 | 99 | 2 B46598 | tropomyosin TPM2 - | |
| 11 | 85 | 9.6 | 161 | 2 S48396 | hypothetical prote | |
| 12 | 82.5 | 9.3 | 163 | 2 F75559 | hypothetical prote | |
| 13 | 79.5 | 9.0 | 135 | 2 S74746 | hypothetical prote | |
| 14 | 79 | 8.9 | 154 | 2 T12720 | hypothetical prote | |
| 15 | 79 | 8.9 | 159 | 2 A97836 | embryonic abundan | |
| 16 | 78.5 | 8.9 | 129 | 2 F64117 | trichohyalin compo | |
| 17 | 78.5 | 8.9 | 141 | 2 C64576 | hypothetical prote | |
| 18 | 78 | 8.8 | 123 | 2 A84228 | hypothetical prote | |
| 19 | 77 | 8.7 | 113 | 2 S66805 | light meromyosin - | |
| 20 | 77 | 8.7 | 142 | 2 I50496 | plasminogen-bindin | |
| 21 | 77 | 8.7 | 147 | 2 S70457 | hypothetical prote | |
| 22 | 77 | 8.7 | 148 | 2 T05610 | hypothetical prote | |
| 23 | 76.5 | 8.6 | 79 | 2 G86722 | gas-vesicle protei | |
| 24 | 76.5 | 8.6 | 162 | 2 B27475 | conserved hypothet | |
| 25 | 76 | 8.6 | 109 | 2 A83265 | hypothetical prote | |
| 26 | 76 | 8.6 | 118 | 2 AD1568 | translocation prot | |
| 27 | 76 | 8.6 | 158 | 2 H83434 | flagella-related p | |
| 28 | 76 | 8.6 | 160 | 2 H75062 | hypothetical prote | |
| 29 | 75.5 | 8.5 | 140 | 2 G72208 | | |

| | | | | | |
|----|------|-----|-----|----------|--------------------|
| 30 | 75 | 8.5 | 114 | 2 B24733 | myosin heavy chain |
| 31 | 75 | 8.5 | 146 | 2 T29401 | hypothetical prote |
| 32 | 74.5 | 8.4 | 133 | 2 C91001 | hypothetical prote |
| 33 | 74.5 | 8.4 | 138 | 2 A83960 | hypothetical prote |
| 34 | 74.5 | 8.4 | 143 | 2 D85846 | unknown protein en |
| 35 | 74.5 | 8.4 | 170 | 2 F72296 | conserved hypothet |
| 36 | 74 | 8.4 | 79 | 2 S53443 | kinetoplastid memb |
| 37 | 74 | 8.4 | 167 | 2 H69881 | hypothetical prote |
| 38 | 73.5 | 8.3 | 137 | 2 T38886 | hypothetical coile |
| 39 | 73.5 | 8.3 | 152 | 2 A53051 | troponin C (Ca(2+) |
| 40 | 73.5 | 8.3 | 163 | 2 D64431 | hypothetical prote |
| 41 | 73.5 | 8.3 | 169 | 2 H96567 | antifreeze protein |
| 42 | 73 | 8.2 | 108 | 2 A59010 | hypothetical prote |
| 43 | 73 | 8.2 | 108 | 2 H71194 | hypothetical prote |
| 44 | 73 | 8.2 | 133 | 2 T33585 | hypothetical prote |
| 45 | 73 | 8.2 | 142 | 2 C22702 | neurofilament trip |

ALIGNMENTS

RESULT 1
S21830
apolipoprotein A-I - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 22-May-1998 #text_change 09-Jul-2004
C;Accession: S21830
R;Trieu, V.N.; Rohwer-Nuttler, P.; Black, D.D.
submitted to the EMBL Data Library, May 1991
A;Description: Sequence and developmental expression of porcine ApoA-I mRNA.
A;Reference number: S21830
A;Accession: S21830
A;Molecule type: mRNA
A;Residues: 1-164 <TRI>
A;Cross-references: UNIPROT:P18648; EMBL:X59414; NID:g1891; PIDN:CAA42050.1; PID:g1892
A;Experimental source: liver
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; li

| | | | | |
|-----------------------|--------|--|-------|----------------------------------|
| Query Match | 41.8%; | Score 370; | DB 2; | Length 164; |
| Best Local Similarity | 79.8%; | Pred. No. 8.5e-17; | | |
| Matches | 71; | Conservative | 7; | Mismatches 11; Indels 0; Gaps 0; |
| | | | | |
| QY | 82 | LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKL | 141 | |
| | | | | |
| Db | 4 | LRQEMSKDLEEVKKVKVQPYLDDFQNKWQEEMETRYRQKMAPLGAEFREGARQKVQELQEKL | 63 | |
| | | | | |
| QY | 142 | SPLGEEMRDRARAHVDALRTHLAPYSDEL | 170 | |
| | | | | |
| Db | 64 | SPLAEELRSRLRAHVEALRQHVAPYSDDL | 92 | |

RESULT 2
S67972
apolipoprotein AI - goose (fragment)
C;Species: Anser anser (domestic goose)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S67972
R;Hermier, D.; Sellier, N.; Rousselot-Pailley, D.; Forgez, P.
Eur. J. Biochem. 234, 586-591, 1995
A;Title: Characterization of apolipoproteins B-100, AI and C from plasma lipoprotein in
A;Reference number: S67972; MUID:96128192; PMID:8536707
A;Accession: S67972
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-34 <HER>
A;Cross-references: UNIPROT:Q9PRR6
C;Superfamily: apolipoprotein A-I

| | | | | | |
|-----------------------|-----|--------------|-----------------|------------|----------------------|
| Query Match | | 12.0%; | Score 106; | DB 2; | Length 34; |
| Best Local Similarity | | 54.5%; | Pred. No. 0.61; | | |
| Matches | 18; | Conservative | 9; | Mismatches | 6; Indels 0; Gaps 0; |

A;Cross-references: UNIPROT:P40414; GB:Z47047; EMBL:Z38059; NID:g603997; PID:g763208; M1
R;Drees, B.; Brown, C.; Barrell, B.G.; Bretscher, A.
J. Cell Biol. 128, 383-392, 1995
A;Title: Tropomyosin is essential in yeast, yet the TPM1 and TPM2 products perform disti
A;Reference number: A56490; MUID:95146545; PMID:7844152
A;Accession: A56490
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-161 <DRE>
A;Cross-references: GB:Z47047; GB:Z38059; NID:g603997; PID:g763208
C;Genetics:
A;Gene: SGD:TPM2
A;Cross-references: SGD:S0001400; MIPS:YIL138c
A;Map position: 9L
C;Superfamily: tropomyosin TPM1
C;Keywords: cytoskeleton

Query Match 9.6%; Score 85; DB 2; Length 161;
Best Local Similarity 22.7%; Pred. No. 70;
Matches 29; Conservative 25; Mismatches 48; Indels 26; Gaps 4;
Qy 27 RYVVSQFEGSALGKQLNLKLLD-NWDSVTSTFSKLREQLGPVTQ--EFWNLKETEGL- 82
|: : : | | | : : : | | | | | | : : |
Db 26 REQLKELEQSNTEKENEIKSLSAKNEQLDSEVEKLESQSDTKQLAEDSNLRSNNENYT 85
Qy 83 --RQEMSKDLEEVKAKVQPYLDDFOK-----KWQEEEMELYRQKVE 120
|: : : | | | : : : | | | : : : | | | : : : |
Db 86 KKNQDLEQLEDSEAKLKEAMDKLKEADLNSEQMGRRIVALEERDEWEKKCEEFQSKYE 145
Qy 121 PLRAELQE 128
: | | |
Db 146 EAQKELDE 153

RESULT 12
F75559
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75559
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75559
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163 <WHI>
A;Cross-references: UNIPROT:Q9RY46; GB:AE001873; GB:AE000513; NID:g6457764; PIDN:AAF0970
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0105
A;Map position: 1

Query Match 9.3%; Score 82.5; DB 2; Length 163;
Best Local Similarity 24.7%; Pred. No. 1e+02;
Matches 24; Conservative 19; Mismatches 51; Indels 3; Gaps 1;
Qy 77 KETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKLHE 136
: | : : : | | | : : : | | | : : : | | | : : : |
Db 30 REMDSANDDLLSGLGQAKHKTDQAAEKVRADTQEAAQNAAREKAQDVRAHVHESAQDFRAG 89
Qy 137 LOEKLSPGCEMRD---RARAHVDAALRTHLAPYSDEL 170
| | : : : | | : | | | | | : : : |
Db 90 AQEQATLRADARDAQAQARDHAQNLRITDVVHEKAQDL 126

RESULT 13
S74746
hypothetical protein slr0978 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.

A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74746
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74746
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-135 <KAN>
A;Cross-references: UNIPROT:P72881; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA1689
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Start codon: GTG
C;Superfamily: Synechocystis hypothetical protein slr0489

Query Match 9.0%; Score 79.5; DB 2; Length 135;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 25; Conservative 20; Mismatches 38; Indels 15; Gaps 3;
Qy 72 WDNLEKETEGLRQEMSKDLEEVKAKV-QPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGA 130
|: : : | | | : : : | | | : : : | | | : : : |
Db 49 WNRNRNRETNLQAQEARVVEGQRRAQERADESRAERERQIARTRIE-----T 99
Qy 131 RQKLHELQEKLSPLGCEMRDRARAHVDALRTHLAPYSD 168
|: : : | | | : | | | : | | | : | | | : | | |
Db 100 RCRIAEIQQLDP-----SDNRRLREALALLAEYGD 132

RESULT 14
T12720
hypothetical protein 4 - Methanobacterium phage psiM2
C;Species: Methanobacterium phage psiM2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12720
R;Pfister, P.; Wasserfallen, A.; Stettler, R.; Leisinger, T.
submitted to the EMBL Data Library, May 1998
A;Description: Archaeophage PsiM2 complete genomic DNA.
A;Reference number: Z17578
A;Accession: T12720
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-154 <PFI>
A;Cross-references: UNIPROT:O80194; EMBL:AF065411; NID:g3249585; PID:g3249589; PIDN:AAC2
A;Experimental source: host Methanobacterium thermoautotrophicum strain Marburg
C;Superfamily: Methanobacterium phage psiM2 hypothetical protein 4

Query Match 8.9%; Score 79; DB 2; Length 154;
Best Local Similarity 26.1%; Pred. No. 1.6e+02;
Matches 31; Conservative 30; Mismatches 40; Indels 18; Gaps 7;
Qy 60 LREQLGPVTQEFWDNLEKTEGLRQ--EMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYR 116
| | : : : | : : : | : : : | : : : | : : : | : : : |
Db 36 LRKNKGIIPELYLKALREELDEISERKIELEKELERLNMB-----EDRLKRELERFS 87
Qy 117 QKV-EPLRAELOEGAR---QKLHELQEKLSPLGCEMRDRARAHVD-ALRTHLAPYSDEL 170
: | | : | | : | | : | | : | | : | | : | | : | | : |
Db 88 EPVDEPMR-EVREARFVNERLEEREGMVSP-SEVVNDRGEDLIEVASRIYGAPEEIL 144

RESULT 15
A97836
hypothetical protein RC1089 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97836
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: A97836
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <KUR>
A;Cross-references: UNIPROT:Q92GN4; GB:AE006914; PIDN:AAL03627.1; PID:g15620212; GSPDB:G
A;Genetics:
A;Gene: RC1089

```
Query Match      8.9%; Score 79; DB 2; Length 159;
Best Local Similarity 24.4%; Pred. No. 1.6e+02;
Matches 19; Conservative 17; Mismatches 42; Indels 0; Gaps 0;
```

| | | | |
|----|----|---|-----|
| Qy | 51 | D S V T S T F S K L R E Q L G P V T Q E F W D N L E K E T E G L R Q E M S K O L E E V K A K V Q P Y L D D F Q K K W Q E | 110 |
| Db | 72 | D K F N Q T L S N T Y D Q I A Q S V T E I K N V K D Q D K K G E E L Q K S I D A V K A M E A V K K A G S K K Q E K | 131 |

| | | | |
|----|-----|--------------------|-----|
| QY | 111 | EMELYRQKVEPLRAELQE | 128 |
| | | : | : |
| | | : | : |
| Db | 132 | IRQHLVDKLEELNKNINE | 149 |

Search completed: December 21, 2004, 10:52:52
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2004, 13:34:52 ; Search time 187 Seconds
(without alignments)
523.068 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_194
Perfect score: 885
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....RARAHVDALRTHLAPYSDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 626041

Minimum DB seq length: 0
Maximum DB seq length: 170

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|---------------------|
| 1 | 320 | 36.2 | 79 | 2 | Q6LD50 | Q6ld50 mus sp. apo |
| 2 | 320 | 36.2 | 79 | 2 | AAB35539 | Aab35539 mus sp. a |
| 3 | 247 | 27.9 | 56 | 2 | O02762 | O02762 ovis aries |
| 4 | 217 | 24.5 | 82 | 2 | Q29248 | Q29248 sus scrofa |
| 5 | 154 | 17.4 | 67 | 2 | Q9Y355 | Q9Y355 homo sapien |
| 6 | 141 | 15.9 | 26 | 2 | Q9UCT8 | Q9uct8 homo sapien |
| 7 | 113 | 12.8 | 155 | 2 | Q6CMT0 | Q6cmt0 kluyveromyc |
| 8 | 111 | 12.5 | 150 | 2 | Q9XDR3 | Q9xdr3 streptococc |
| 9 | 110.5 | 12.5 | 138 | 2 | Q9S6I3 | Q9s6i3 streptococc |
| 10 | 106 | 12.0 | 34 | 2 | Q9PRR6 | Q9prrr6 anser anser |
| 11 | 103 | 11.6 | 143 | 1 | LEA1_APHAV | Q95v77 aphelenchus |
| 12 | 101.5 | 11.5 | 107 | 1 | APE_MACMU | Q28502 macaca mula |
| 13 | 101 | 11.4 | 20 | 1 | APAI_ERYPA | P18647 erythrocebu |
| 14 | 101 | 11.4 | 30 | 2 | Q9QV04 | Q9qv04 rattus sp. |
| 15 | 99 | 11.2 | 107 | 1 | APE_SAI5C | Q28995 saimiri sci |
| 16 | 98.5 | 11.1 | 129 | 2 | Q8ZX78 | Q8zx78 pyrobaculum |
| 17 | 98 | 11.1 | 117 | 2 | Q6QZ11 | Q6qzi1 pseudopleur |
| 18 | 98 | 11.1 | 117 | 2 | AAT01918 | Aat01918 pseudople |
| 19 | 98 | 11.1 | 118 | 2 | O07516 | O07516 bacillus su |
| 20 | 97 | 11.0 | 96 | 2 | Q8RH51 | Q8rh51 fusobacteri |
| 21 | 95.5 | 10.8 | 163 | 2 | Q9R0H4 | Q9r0h4 rattus norv |
| 22 | 94 | 10.6 | 166 | 2 | Q63297 | Q63297 rattus norv |
| 23 | 93.5 | 10.6 | 163 | 2 | Q9ZFL1 | Q9zfl1 streptococc |
| 24 | 92.5 | 10.5 | 102 | 2 | Q98TJ9 | Q98tj9 platichthys |
| 25 | 92.5 | 10.5 | 148 | 2 | Q84MC4 | Q84mc4 arabidopsis |
| 26 | 92 | 10.4 | 114 | 2 | Q6T257 | Q6t257 crassostrea |
| 27 | 92 | 10.4 | 114 | 2 | AAR17060 | Aar17060 crassostr |
| 28 | 92 | 10.4 | 168 | 2 | Q9AGA2 | Q9aga2 streptococc |
| 29 | 90.5 | 10.2 | 164 | 2 | Q9XUV5 | Q9xuv5 caenorhabdi |
| 30 | 90 | 10.2 | 146 | 2 | Q9UWV7 | Q9uwv7 sulfolobus |
| 31 | 89 | 10.1 | 168 | 2 | Q9SR63 | Q9sr63 arabidopsis |

| | | | | | | |
|----|------|------|-----|---|------------|--------------------|
| 32 | 88.5 | 10.0 | 161 | 2 | Q6FKV5 | Q6fkv5 candida gla |
| 33 | 88 | 9.9 | 96 | 2 | Q7P280 | Q7p280 fusobacteri |
| 34 | 88 | 9.9 | 121 | 2 | Q6YQ37 | Q6yq37 onion yello |
| 35 | 88 | 9.9 | 121 | 2 | BAD04623 | Bad04623 onion yel |
| 36 | 88 | 9.9 | 122 | 1 | Y5B6_METAC | Q8tin0 methanosarc |
| 37 | 88 | 9.9 | 129 | 2 | Q8DPA5 | Q8dpa5 streptococc |
| 38 | 88 | 9.9 | 129 | 2 | Q97Q21 | Q97q21 streptococc |
| 39 | 87.5 | 9.9 | 170 | 2 | Q74MC1 | Q74mc1 nanoarchaeu |
| 40 | 87.5 | 9.9 | 170 | 2 | AAR39327 | Aar39327 nanoarcha |
| 41 | 87 | 9.8 | 118 | 2 | O68959 | O68959 streptococc |
| 42 | 87 | 9.8 | 158 | 2 | Q9RN96 | Q9rn96 streptococc |
| 43 | 87 | 9.8 | 170 | 2 | Q72JB9 | Q72jb9 thermus the |
| 44 | 87 | 9.8 | 170 | 2 | AAS81203 | Aas81203 thermus t |
| 45 | 86.5 | 9.8 | 99 | 2 | Q9PSS3 | Q9pss3 gallus gall |

ALIGNMENTS

| | | | | | | | | | |
|--|--|---|------|------|-----|------------------|--------|--|--|
| RESULT 1 | | | | | | | | | |
| Q6LD50 | | | | | | | | | |
| ID | Q6LD50 | PRELIMINARY; | PRT; | 79 | AA. | | | | |
| AC | Q6LD50; | | | | | | | | |
| DT | 05-JUL-2004 | (TrEMBLrel. 27, Created) | | | | | | | |
| DT | 05-JUL-2004 | (TrEMBLrel. 27, Last sequence update) | | | | | | | |
| DT | 05-JUL-2004 | (TrEMBLrel. 27, Last annotation update) | | | | | | | |
| DE | Apolipoprotein A1 homolog protein (Fragment). | | | | | | | | |
| GN | Name=apolipoprotein A1 homolog; | | | | | | | | |
| OS | Mus sp. | | | | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | | | | | |
| OX | NCBI_TaxID=10095; | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RX | MEDLINE=96062440; PubMed=7488287; | | | | | | | | |
| RA | Merrill J.T., Rivkin E., Shen C., Lahita R.G.; | | | | | | | | |
| RT | "Selection of a gene for apolipoprotein A1 using autoantibodies from a | | | | | | | | |
| RT | patient with systemic lupus erythematosus."; | | | | | | | | |
| RL | Arthritis Rheum. 38:1655-1659(1995). | | | | | | | | |
| DR | EMBL; S80442; AAB35539.1; -- | | | | | | | | |
| DR | InterPro; IPR009074; Apolipo_A_E_C3. | | | | | | | | |
| KW | Lipoprotein. | | | | | | | | |
| FT | NON_TER | 79 | 79 | | | | | | |
| SQ | SEQUENCE | 79 | AA; | 9583 | MW; | 33CA72DA854A150A | CRC64; | | |
| Query Match 36.2%; Score 320; DB 2; Length 79; | | | | | | | | | |
| Best Local Similarity 76.9%; Pred. No. 3.9e-13; | | | | | | | | | |
| Matches 60; Conservative 10; Mismatches 8; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 70 | EFWNLKETETGLRQEMSKDLEEVKAKVQPYLDDFQKKQOEEMELYRQKVEPLRAELQEG 129 | | | | | | | |
| Db | 1 | DFWNLKETDWRQEMNKDLEEVKQKVQPYLDEFQKKWKEDVELYRQKVAPLGAELQES 60 | | | | | | | |
| QY | 130 | ARQKLHELQEKLSPLGEE 147 | | | | | | | |
| Db | 61 | ARQKLQELQGRLLSPVAEE 78 | | | | | | | |
| RESULT 2 | | | | | | | | | |
| AAB35539 | | | | | | | | | |
| ID | AAB35539 | PRELIMINARY; | PRT; | 79 | AA. | | | | |
| AC | AAB35539; | | | | | | | | |
| DT | 02-MAR-2004 | (TrEMBLrel. 27, Created) | | | | | | | |
| DT | 02-MAR-2004 | (TrEMBLrel. 27, Last sequence update) | | | | | | | |
| DT | 02-MAR-2004 | (TrEMBLrel. 27, Last annotation update) | | | | | | | |
| DE | Apolipoprotein A1 homolog (Fragment). | | | | | | | | |
| OS | Mus sp. | | | | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | | | | | |
| OX | NCBI_TaxID=10095; | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RX | MEDLINE=96062440; PubMed=7488287; | | | | | | | | |

RA Merrill J.T., Rivkin E., Shen C., Lahita R.G.;
RT "Selection of a gene for apolipoprotein A1 using autoantibodies from a
RT patient with systemic lupus erythematosus."
RL Arthritis Rheum. 38:1655-1659(1995).
DR EMBL; S80442; AAB35539.1; --.
FT NON_TER 1 1
SQ SEQUENCE 79 AA; 9583 MW; 33CA72DA854A150A CRC64;

Query Match 36.2%; Score 320; DB 2; Length 79;
Best Local Similarity 76.9%; Pred. No. 3.9e-13;
Matches 60; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 70 EFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEG 129
:|||||: :|||:||||| :|||:||||| :|||:||||| :|||:||||| :|||:|||||
Db 1 DFWDNLEKETDWRQEMNKDLEEVKQKQVQPYLDEFQKKWKEDVELYRQKVAPLGAELQES 60

Qy 130 ARQKLHELQKLSPLGEE 147
||||| :|||:||||| :|||:||||| :|||:||||| :|||:||||| :|||:|||||
Db 61 ARQKLQELQGRLSPVAAE 78

RESULT 3
O02762 PRELIMINARY; PRT; 56 AA.
ID O02762
AC O02762;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99098454; PubMed=9883985;
RA Robertson J.A., Bhattacharyya S., Ing N.H.;
RT "Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and
RT glyceroldehyde 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";
RL J. Steroid Biochem. Mol. Biol. 67:285-292(1998).
DR EMBL; U94720; AAB57840.1; --.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 1 1
FT NON_TER 56 56
SQ SEQUENCE 56 AA; 6617 MW; 2AB38E08F1E8F1BC CRC64;

Query Match 27.9%; Score 247; DB 2; Length 56;
Best Local Similarity 82.1%; Pred. No. 1e-08;
Matches 46; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 47 LDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 102
|||||: |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LDNWDSLASTLSKVRQLGPVTQEFWDNLEKETASLRQEMHKDLEEARQKVQPYLD 56

RESULT 4
Q29248 PRELIMINARY; PRT; 82 AA.
ID Q29248
AC Q29248;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library."
RL Mamm. Genome 7:509-517(1996).
DR EMBL; F14858; CAA23298.1; --.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9168 MW; 24625C65CBFFEDD8 CRC64;

Query Match 24.5%; Score 217; DB 2; Length 82;
Best Local Similarity 70.7%; Pred. No. 1.2e-06;
Matches 41; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQEGSALGKQLKLLDNWDSVTSTFSK 59
:|||||: |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 DDPXSPWDRVKDFXTVYVDAIKDSGRDYXAQFEASALGKHLNKLKLNKXDSLXTFTK 82

RESULT 5
Q9Y355 PRELIMINARY; PRT; 67 AA.
ID Q9Y355
AC Q9Y355;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99216322; PubMed=10198255;
RA Hamidi Asl K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;
RT "A novel apolipoprotein A-1 variant, Arg173Pro, associated with
RT cardiac and cutaneous amyloidosis.";
RL Biochem. Biophys. Res. Commun. 257:584-588(1999).
DR EMBL; AF148963; AAD34604.1; --.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 1 1
FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7433 MW; 525E1FEB7BDD5AFB CRC64;

Query Match 17.4%; Score 154; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 LSPGLGEEMRDRARAHVDALRTHLAPYSDEL 170
|||||: |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LSPGLGEEMRDRARAHVDALRTHLAPYSDEL 30

RESULT 6

RT "Cerebrovascular amyloidosis in squirrel monkeys and rhesus monkeys:
RT apolipoprotein E genotype.";
RL FEBS Lett. 379:132-134(1996).
CC -!- FUNCTION: Mediates the binding, internalization, and catabolism of
CC lipoprotein particles. It can serve as a ligand for the LDL (apo
CC B/E) receptor and for the specific apo-E receptor (chylomicron
CC remnant) of hepatic tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Secreted in plasma.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U52029; AAC50442.1; -.
DR HSSP; P02649; INFN.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
KW Plasma; Repeat; VLDL.
FT NON_TER 1 1 LDL receptor binding (Potential).
FT DOMAIN 89 99 Heparin-binding (By similarity).
FT DOMAIN 93 96 8 X 22 AA approximate tandem repeats.
FT DOMAIN 11 >107 1.
FT REPEAT 11 32 2.
FT REPEAT 33 54 3.
FT REPEAT 55 76 4.
FT REPEAT 77 98 5.
FT REPEAT 99 >107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12328 MW; FF88CED47BD18F7C CRC64;

Query Match 11.2%; Score 99; DB 1; Length 107;
Best Local Similarity 26.2%; Pred. No. 41;
Matches 27; Conservative 19; Mismatches 35; Indels 22; Gaps 1;

Qy 58 SKLREQILGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQ 117
Db 25 SELEEQLSPVAETRARLSKELQAAQARLGADMEDVRSRLAQY----- 67

Qy 118 KVEPLRAELQEGARQKLHELQELKSLPLGEEMRDRARAHVDALR 160
Db 68 -----RSEVQAMLGQSTDELRLARLASHLRKLRKLLRDVDDLQ 105

Search completed: December 21, 2004, 13:51:30
Job time : 190 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 10:45:04 ; Search time 66 Seconds
(without alignments)
924.000 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_194
Perfect score: 885
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....RARAHVDAALRTHLAPYSDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1323736

Minimum DB seq length: 0
Maximum DB seq length: 170

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 885 | 100.0 | 170 | 6 | ADA61215 Human 18K |
| 2 | 727 | 82.1 | 151 | 4 | AAO02278 Human pol |
| 3 | 647.5 | 73.2 | 166 | 4 | AAU28372 Novel hum |
| 4 | 612 | 69.2 | 160 | 6 | ABP75964 Human GEN |
| 5 | 529.5 | 59.8 | 168 | 5 | AAE24649 Human MSP |
| 6 | 501.5 | 56.7 | 154 | 4 | AAO12095 Human pol |
| 7 | 479.5 | 54.2 | 119 | 4 | AAU30468 Novel hum |
| 8 | 476.5 | 53.8 | 120 | 4 | AAU30469 Novel hum |
| 9 | 476.5 | 53.8 | 120 | 4 | AAU30267 Novel hum |
| 10 | 442.5 | 50.0 | 168 | 5 | AAE24648 Human MSP |
| 11 | 437 | 49.4 | 158 | 7 | ADJ70395 Human hea |
| 12 | 218 | 24.6 | 42 | 2 | AAR20164 Apo AI po |
| 13 | 197 | 22.3 | 65 | 6 | ABP76131 Human GEN |
| 14 | 163 | 18.4 | 32 | 2 | AAR20165 Apo AI po |
| 15 | 162 | 18.3 | 64 | 5 | ABP31744 Human apo |
| 16 | 138 | 15.6 | 26 | 4 | AAG62609 Apolipop |
| 17 | 137 | 15.5 | 26 | 7 | ADE76474 ApoAI G* |
| 18 | 123 | 13.9 | 85 | 8 | ADP87441 Monkey ap |
| 19 | 119 | 13.4 | 85 | 8 | ADP87442 Human apo |
| 20 | 119 | 13.4 | 85 | 8 | ADP87440 Baboon ap |
| 21 | 118 | 13.3 | 22 | 1 | AAP2072 Apolipop |
| 22 | 118 | 13.3 | 107 | 8 | ADP87432 Rat apoli |
| 23 | 116 | 13.1 | 21 | 1 | AAP90956 Apo AI ep |
| 24 | 115 | 13.0 | 107 | 8 | ADP87431 Rat apoli |
| 25 | 111 | 12.5 | 22 | 4 | AAG62608 Apolipop |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 26 | 109 | 12.3 | 107 | 8 | ADP87437 | Adp87437 Mouse apo |
| 27 | 109 | 12.3 | 107 | 8 | ADP87433 | Adp87433 Mouse apo |
| 28 | 109 | 12.3 | 107 | 8 | ADP87436 | Adp87436 Mouse apo |
| 29 | 109 | 12.3 | 107 | 8 | ADP87434 | Adp87434 Mouse apo |
| 30 | 108 | 12.2 | 84 | 2 | AAy42554 | Aay42554 Apolipop |
| 31 | 107 | 12.1 | 85 | 8 | ADP87438 | Adp87438 Chicken a |
| 32 | 107 | 12.1 | 85 | 8 | ADP87439 | Adp87439 Pig apoli |
| 33 | 106.5 | 12.0 | 107 | 2 | AAR32705 | Aar32705 SSP-534 p |
| 34 | 106.5 | 12.0 | 107 | 2 | AAR78265 | Aar78265 Synthetic |
| 35 | 106.5 | 12.0 | 107 | 2 | AAW87756 | Aaw87756 Synthetic |
| 36 | 106.5 | 12.0 | 107 | 6 | ADA15988 | Ada15988 Synthetic |
| 37 | 106.5 | 12.0 | 107 | 6 | ABO44352 | AbO44352 Ear I-bas |
| 38 | 102 | 11.5 | 107 | 8 | ADP87435 | Adp87435 Mouse apo |
| 39 | 101 | 11.4 | 110 | 2 | AAR12387 | Aar12387 Amplified |
| 40 | 97.5 | 11.0 | 97 | 8 | ADP87414 | Adp87414 CF11428 s |
| 41 | 97 | 11.0 | 19 | 1 | AAP92073 | Aap92073 Apolipop |
| 42 | 96.5 | 10.9 | 95 | 6 | ABP70773 | Abp70773 Human apo |
| 43 | 96.5 | 10.9 | 96 | 8 | ADP87419 | Adp87419 Tupala gl |
| 44 | 94 | 10.6 | 18 | 7 | ADC29635 | Adc29635 Antioxi |
| 45 | 94 | 10.6 | 30 | 7 | ADC29665 | Adc29665 Antioxi |

ALIGNMENTS

RESULT 1
ADA61215
ID ADA61215 standard; protein; 170 AA.
XX
AC ADA61215;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human 18K apolipoprotein A-1 (apo-A-1) fragment.
XX

KW Human; apolipoprotein A-I; apo-A-I; T-cell activation inhibitor-like;
KW APTI; T-cell-mediated activation; monocyte; interleukin-1beta; IL-1beta;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy;
KW IL-1-mediated disease; acute pancreatitis; Alzheimer's disease; asthma;
KW cancer; diabetes; glomerulonephritis; multiple sclerosis; osteoporosis;
KW pain; Parkinson's disease; psoriasis; uveitis; TNF-mediated disease;
KW depression; pancreatitis; periodontal disease; pulmonary fibrosis;
KW reperfusion injury; rheumatic disease; septic shock;
KW systemic lupus erythematosus; thyroiditis; neutropenic; neuroprotective;
KW cytostatic; nephrotropic; analgesic; ophthalmological; antiinflammatory;
KW vasotropic; antibacterial; immunosuppressive; dermatological.

XX Homo sapiens.
OS
XX US2002064820-A1.
XX
XX 30-MAY-2002.
XX
XX 13-MAR-2001; 2001US-00803918.
XX
XX 13-MAR-2000; 2000US-0189008P.
XX 31-MAR-2000; 2000US-0193551P.
XX
XX (DAYE/) DAYER J.
XX (BURG/) BURGER D.
XX (KOHN/) KOHNO T.
XX (EDWA/) EDWARDS C K.

PI Dayer J, Burger D, Kohno T, Edwards CK;
XX
XX WPI; 2003-615701/58.
XX N-PSDB; ADA61216.

XX
XX New apolipoprotein A-I polypeptide or its related polypeptide termed apo-
XX A-I fragment T-cell activation inhibitor-like polypeptide, useful for
XX treating interleukin-1 or tumor necrosis factor-alpha mediated disease.
XX
XX Claim 15; Fig 1B; 56pp; English.

XX The invention discloses a apolipoprotein A-I (apo-A-I) polypeptide or its
CC related polypeptide, apo-A-I fragment T-cell activation inhibitor-like
CC (AFTI) polypeptide, or a fragment or an allelic or splice variant. Apo-A-
CC I and its derivatives are used in regulating T-cell-mediated activation
CC of monocytes. Also disclosed is an antibody produced by immunising an
CC animal with apo-A-I and a selective binding agent, or its fragment. Apo-A
CC -I is useful for reducing inflammation, interleukin (IL)-1beta secretion
CC or tumour necrosis factor (TNF)-alpha secretion in a subject, or for
CC treating IL-1 or TNF-alpha mediated disease in a subject. The
CC compositions of the invention are useful for treating (e.g. gene
CC therapy), preventing or ameliorating a medical condition involving
CC monocyte activation in a patient, for determining whether a compound
CC inhibits activity or production of apo-A-I, for detecting or quantifying
CC the amount of apo-A-I in a sample, for regulating T-cell-mediated
CC activation of monocytes, to identify a molecule that binds to apo-A-I,
CC for identifying AFTI receptors, for cloning AFTI receptors, and as an
CC immunogen to raise antibodies, for treating acute and chronic IL-1-
CC mediated diseases such as acute pancreatitis, Alzheimer's disease,
CC asthma, cancer, diabetes, glomerulonephritis, multiple sclerosis,
CC osteoporosis, pain, Parkinson's disease, psoriasis, uveitis, and acute
CC and chronic TNF-mediated diseases such as depression, pancreatitis,
CC periodontal diseases, pulmonary fibrosis, reperfusion injury, rheumatic
CC diseases, septic shock, systemic lupus erythematosus and thyroiditis.
CC They are also useful for regulating expression and modulating levels of
CC apo-A-I, as hybridisation probes in diagnostic assays, for diagnostic
CC applications, to test for the presence of apo-A-I in cells, for in vivo
CC imaging and in therapeutics. The sequence presented is the human 18K N-
CC terminal apo-A-1 protein fragment.

XX
SQ Sequence 170 AA;

Query Match 100.0%; Score 885; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.8e-66;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEPPQSPWDRVKDLATVYVDLVKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60
Db 1 DEPPQSPWDRVKDLATVYVDLVKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60

Qy 61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120
Db 61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120

Qy 121 PLRAELQEGARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDEL 170
Db 121 PLRAELQEGARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDEL 170

RESULT 2
AAO02278
ID AAO02278 standard; protein; 151 AA.
XX
AC AAO02278;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 16170.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.

PR 18-MAY-2000; 2000US-00577409.
XX (HYSE-) HYSEQ INC.
PA
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI92209.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 20; SEQ ID NO 16170; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 151 AA;

Query Match 82.1%; Score 727; DB 4; Length 151;
Best Local Similarity 94.0%; Pred. No. 1.1e-52;
Matches 140; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 22 LKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEG 81
Db 1 LKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEG 60

Qy 82 LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKL 141
Db 61 LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKL 120

Qy 142 SPLGEEMDRARAHVDALRTHLAPYSDEL 170
Db 121 SPLGEEMDRARAHVDALRTHMAPYSDEL 149

RESULT 3
AAU28372
ID AAU28372 standard; protein; 166 AA.
XX
AC AAU28372;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secretory protein, Seq ID No 729.
XX
KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.
XX
OS Homo sapiens.
XX
PN WO200166689-A2.
XX
PD 13-SEP-2001.
XX

DE Human MSP1D5-6 (helices 5 and 6 deleted) protein.
XX
KW Human; membrane scaffold protein; MSP; phospholipid; nanoscale particle;
KW hydrogel; gold biosensor surface; reproducible assay; crystallisation;
KW biotechnology; pharmaceutical industry; structure determination;
KW bioseparation; drug discovery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200240501-A2.
XX
PD 23-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043451.
XX
PR 20-NOV-2000; 2000US-0252233P.
XX
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Sligar SG, Bayburt TH;
XX
DR WPI; 2002-500201/53.
DR N-PSDB; AAD39711.
XX
PT New membrane scaffold protein for forming nanoscale particles, useful in
PT biological research, self assembles with(out) phospholipids into a
PT nanoscale particle in an aqueous environment.
XX
PS Claim 8; Page 39; 112pp; English.
XX
CC The invention relates to a membrane scaffold protein (MSP), that self
CC assembles in the absence of phospholipid, with a phospholipid or a
CC mixture of phospholipids, into a nanoscale particle of 5-500 nm in
CC diameter, in an aqueous environment, where the membrane scaffold protein
CC is amphipathic and forms at least one alpha helix. The nanoscale particle
CC comprising MSP is useful for identifying a competitor of binding of a
CC ligand to a receptor protein which is incorporated within the nanoscale
CC particle together with MSP, by contacting nanoscale particle and a
CC receptor protein with a detectable ligand to produce nanoscale particle-
CC bound detectable ligand, contacting the bound ligand with a test
CC compound, and measuring detectable ligand released from the particle,
CC such that a competitor of ligand binding is identified when contacting
CC the bound ligand results in release of the detectable ligand. The
CC invention is useful for the incorporation of additional hydrophobic or
CC partially hydrophobic protein molecules. The nanoscale particle can form
CC tags for purification and physical manipulation of disks such as in
CC hydrogels on or a gold biosensor surface, and they can serve as entities
CC for rapid and reproducible assay and crystallisation. The nanoscale
CC particle and MSP are useful in biotechnology, pharmaceutical industries
CC and in research areas. The nanoscale particle is useful for structure/
CC function correlation, structure determination, bioseparation and drug
CC discovery. The present sequence is MSP1D5-6 protein
XX
SQ Sequence 168 AA;
Query Match 59.8%; Score 529.5; DB 5; Length 168;
Best Local Similarity 74.5%; Pred. No. 3.4e-36;
Matches 108; Conservative 5; Mismatches 25; Indels 7; Gaps 1;
QY 26 GRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSLREQLGPVTQEFWDNLEKETEGLRQE 85
| : ||
2 GHHHHHHIEG-----RLKLLDNWDSVTSTFSLREQLGPVTQEFWDNLEKETEGLRQE 54
Db
QY 86 MSKOLEEVKAKVQPYLDDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQKLSPLG 145
|||||
55 MSKOLEEVKAKVQPYLDDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQKLSARL 114
QY 146 EEMRDRARAHVDALRTHLAPYSDEL 170
| : | : | : :
Db 115 AEYHAKATEHLSTLSEKAKPALEDL 139

RESULT 6
AAO12095
ID AAO12095 standard; protein; 154 AA.
XX
AC AAO12095;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 25987.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US0004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI92026.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 20; SEQ ID NO 25987; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 154 AA;
Query Match 56.7%; Score 501.5; DB 4; Length 154;
Best Local Similarity 79.5%; Pred. No. 6.6e-34;
Matches 97; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
QY 1 DEFPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSL 60
|||||
33 DEFPQSPWDRVMDLATAYVDGLKDSGRDYASQFEGYALGKQLNMLLDNWDSTVYTFSL 92
QY 61 REQLGPVTQEFWDNLEKETEGLRQEMSKOLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120
|||||
93 REQLGPVTQEFWDNLDKETEGLTHEMSKOLEEDVNAKVQTYLYDFQKTQKEL-TFTAES 151
121 PL 122
Db 152 PV 153
RESULT 7
AAU30468

ID AAU30468 standard; protein; 119 AA.
XX
AC AAU30468;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #959.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 297; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 119 AA;

Query Match 54.2%; Score 479.5; DB 4; Length 119;
Best Local Similarity 89.0%; Pred. No. 3.3e-32;
Matches 97; Conservative 1; Mismatches 6; Indels 5; Gaps 1;

QY 43 NLKLLDNWDSVTSTFSSKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLD 102
Db
2 NLKLLDNWDSVTSTFSSKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLD 61

QY 103 DFQKKWQEEEMELYRQKVEPLRAELQEGAROKLHELQEK-----LSPLGE 146
Db 62 DFQKKWQEEEMELYRQKVEPLRAELQEGAROKLLPVLESFKVSFLSALEE 110

RESULT 8
AAU30469
ID AAU30469 standard; protein; 120 AA.
XX
AC AAU30469;
XX

DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #960.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 297; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 120 AA;

Query Match 53.8%; Score 476.5; DB 4; Length 120;
Best Local Similarity 79.7%; Pred. No. 5.9e-32;
Matches 94; Conservative 1; Mismatches 0; Indels 23; Gaps 1;

QY 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60
Db
25 DEPPQSPWDRVKDLATVYVDVLKDSGK-----DSVTSTFSKL 61

QY 61 REQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLDDFFQKKWQEEEMELYRQK 118
Db 62 REQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLDDFFQKKWQEEEMELYRQK 119

RESULT 9
AAU30267
ID AAU30267 standard; protein; 120 AA.
XX
AC AAU30267;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #758.
XX

KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 270; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 120 AA;

Query Match 53.8%; Score 476.5; DB 4; Length 120;
Best Local Similarity 79.7%; Pred. No. 5.9e-32;
Matches 94; Conservative 1; Mismatches 0; Indels 23; Gaps 1;

Qy 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60
Db 25 DEPPQSPWDRVKDLATVYVDVLKDSGK-----DSVTSTFSKL 61

Qy 61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQK 118
Db 62 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQK 119

RESULT 10
AAE24648
ID AAE24648 standard; protein; 168 AA.
XX
AC AAE24648;
XX
DT 22-OCT-2002 (first entry)
XX
DE Human MSP1D4-5 (helices 4 and 5 deleted) protein.
XX
KW Human; membrane scaffold protein; MSP; phospholipid; nanoscale particle;
KW hydrogel; gold biosensor surface; reproducible assay; crystallisation;
KW biotechnology; pharmaceutical industry; structure determination;
KW bioseparation; drug discovery.

XX Homo sapiens.
OS Synthetic.
XX
PN WO200240501-A2.
XX
PD 23-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043451.
XX
PR 20-NOV-2000; 2000US-0252233P.
XX
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Sligar SG, Bayburt TH;
XX
DR WPI; 2002-500201/53.
DR N-PSDB; AAD39706.
XX
XX New membrane scaffold protein for forming nanoscale particles, useful in
PT biological research, self assembles with(out) phospholipids into a
PT nanoscale particle in an aqueous environment.
XX
PS Claim 8; Page 38; 112pp; English.
XX
CC The invention relates to a membrane scaffold protein (MSP), that self
CC assembles in the absence of phospholipid, with a phospholipid or a
CC mixture of phospholipids, into a nanoscale particle of 5-500 nm in
CC diameter, in an aqueous environment, where the membrane scaffold protein
CC is amphipathic and forms at least one alpha helix. The nanoscale particle
CC comprising MSP is useful for identifying a competitor of binding of a
CC ligand to a receptor protein which is incorporated within the nanoscale
CC particle together with MSP, by contacting nanoscale particle and a
CC receptor protein with a detectable ligand to produce nanoscale particle-
CC bound detectable ligand, contacting the bound ligand with a test
CC compound, and measuring detectable ligand released from the particle,
CC such that a competitor of ligand binding is identified when contacting
CC the bound ligand results in release of the detectable ligand. The
CC invention is useful for the incorporation of additional hydrophobic or
CC partially hydrophobic protein molecules. The nanoscale particle can form
CC tags for purification and physical manipulation of disks such as in
CC hydrogels on or a gold biosensor surface, and they can serve as entities
CC for rapid and reproducible assay and crystallisation. The nanoscale
CC particle and MSP are useful in biotechnology, pharmaceutical industries
CC and in research areas. The nanoscale particle is useful for structure/
CC function correlation, structure determination, bioseparation and drug
CC discovery. The present sequence is MSP1D4-5
XX
SQ Sequence 168 AA;

Query Match 50.0%; Score 442.5; DB 5; Length 168;
Best Local Similarity 63.4%; Pred. No. 6e-29;
Matches 92; Conservative 9; Mismatches 37; Indels 7; Gaps 1;

Qy 26 GRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE 85
Db 2 GHHHHHHIEG-----RLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE 54

Qy 86 MSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
Db 55 MSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPYSDELRLQRLAARLEALKENGARL 114

Qy 146 EEMRDRARAHVDALRTHLAPYSDEL 170
Db 115 AEYHAKATEHLSTLSEKAKPALEDL 139

RESULT 11
ADJ70395
ID ADJ70395 standard; protein; 158 AA.
XX
AC ADJ70395;
XX

DT 06-MAY-2004 (first entry)
XX Human heat mitochondrial protein as a therapeutic target SeqID2201.
DE
XX
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
XX WO2003087768-A2.
XX
XX 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 2201; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 158 AA;

Query Match 49.4%; Score 437; DB 7; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.6e-28;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 MSKDLEEVKAKVQPYLDDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
Db 1 MSKDLEEVKAKVQPYLDDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 60

QY 146 EEMRDRARAHVDALRTHLAPYSDEL 170
Db 61 EEMRDRARAHVDALRTHLAPYSDEL 85

RESULT 12
AAR20164
ID AAR20164 standard; peptide; 42 AA.

XX AAR20164;
AC
XX 25-MAR-2003 (revised)
DT 01-APR-1992 (first entry)
XX
DE Apo AI polypeptide (A).
XX Monoclonal antibody; MAB AI-11; epitope; diagnosis.
KW
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Peptide 1. .28
FT Peptide 2. .28
FT Peptide 7. .28
FT Peptide 10. .28
FT Peptide 11. .42
FT Peptide 11. .28
FT Peptide 13. .28
XX WO9118619-A.
PN
XX 12-DEC-1991.
PD
XX 07-JUN-1990; 90US-00534761.
PF
XX 07-JUN-1990; 90US-00534761.
PR
XX (SCRI) SCRIPPS CLINIC & RES.
XX
PI Curtiss LK, Banka CL, Bonnet DJ, Smith RS;
XX
DR WPI; 1992-007201/01.
XX
PT New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo AI
PT in vascular fluid samples and increase LCAT-mediated cholesterol
PT esterification in humans.
XX
PS Claim 2; Page 68; 87pp; English.
XX
CC The peptides represented in AAR20164-65 are capable of immunologically
CC mimicking an Apo AI epitope. They are useful in diagnosis and detection
CC of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is
CC useful in therapeutic methods for increasing LCAT- mediated cholesterol
CC esterification in humans. The Apo AI polypeptide is selected from the
CC peptides indicated in the features and includes amino acids 13-28
CC defining a conserved native epitope on Apo AI capable of immunoreacting
CC with monoclonal antibody MAB AI-11. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 42 AA;

Query Match 24.6%; Score 218; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 5.4e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 QEMSKDLEEVKAKVQPYLDDDFQKKWQEEEMELYRQKVEPLRAE 125
Db 1 QEMSKDLEEVKAKVQPYLDDDFQKKWQEEEMELYRQKVEPLRAE 42

RESULT 13
ABP76131
ID ABP76131 standard; protein; 65 AA.
XX
AC ABP76131;
XX
DT 21-FEB-2003 (first entry)
XX
DE Human GENSET protein SEQ ID 457.
KW Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;

KW gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;
KW inflammatory disease; immune disorder; neuromuscular; toxicity;
KW central nervous system; cardiovascular; gastrointestinal.
XX Homo sapiens.
OS
XX WO200283898-A1.
PN
XX
XX
PD 24-OCT-2002.
XX
PF 18-APR-2001; 2001WO-IB0000914.
XX
PR 18-APR-2001; 2001WO-IB0000914.
XX
XX (GEST) GENSET.
PA
XX Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;
PI WPI; 2003-075548/07.
DR
XX
XX New GENSET polynucleotides and polypeptides, useful for treating heavy
PT metal toxicity, cancer, inflammatory diseases, immune disorders, and the
PT neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
PT toxicity.
XX
XX Claim 14; Page 535; 735pp; English.
PS
XX The present invention relates to novel GENSET polynucleotides (ABZ36404-
CC ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides
CC and polypeptides are useful in screening and diagnostic assays for
CC abnormal GENSET expression and/or biological activity. They are also
CC useful for screening of compounds for treating or preventing GENSET-
CC related disorders, such as heavy metal toxicity, cancer, inflammatory
CC diseases, immune disorders, and the neuromuscular, central nervous system
CC (CNS), cardiovascular or gastrointestinal effects of the toxicity
XX
SQ Sequence 65 AA;

Query Match 22.3%; Score 197; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 5.2e-09;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 37
Db
25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 61

RESULT 14
AAR20165
ID . AAR20165 standard; protein; 32 AA.
XX
AC AAR20165;
XX
DT 25-MAR-2003 (revised)
DT 01-APR-1992 (first entry)
XX
DE Apo AI polypeptide (B).
XX
XX Monoclonal antibody; MAB AI-14; epitope; diagnosis.
KW
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .32
FT Peptide 1. .21
FT Peptide 5. .28
FT Peptide 5. .21
FT Peptide 6. .28
FT Peptide 6. .21
FT Misc-difference 11
FT /label= GLU, PHE
XX
PN WO9118619-A.

XX 12-DEC-1991.
PD
XX
XX 07-JUN-1990; 90US-00534761.
PF
XX
XX 07-JUN-1990; 90US-00534761.
PR
XX
XX (SCRI) SCRIPPS CLINIC & RES.
PA
XX
XX Curtiss LK, Banka CL, Bonnet DJ, Smith RS;
PI
XX
XX WPI; 1992-007201/01.
DR
XX
XX New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo AI
PT in vascular fluid samples and increase LCAT-mediated cholesterol
PT esterification in humans.
XX
XX Claim 5; Page 68; 87pp; English.
PS
XX The peptides represented in AAR20164-65 are capable of immunologically
CC mimicking an Apo AI epitope. They are useful in diagnosis and detection
CC of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is
CC useful in therapeutic methods for increasing LCAT- mediated cholesterol
CC esterification in humans. The Apo AI polypeptide is selected from the
CC peptides indicated in the features and includes amino acids 6-21 defining
CC a conserved native epitope on Apo AI capable of immunoreacting with
CC monoclonal antibody MAB AI-4. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 32 AA;

Query Match 18.4%; Score 163; DB 2; Length 32;
Best Local Similarity 96.9%; Pred. No. 1.5e-06;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 94 KAKVQPYLDDDFQKKWQEMELYRQKVEPLRAE 125
Db 1 KAKVQPYLDDXQKKWQEMELYRQKVEPLRAE 32

RESULT 15
ABP31744
ID ABP31744 standard; protein; 64 AA.
XX
AC ABP31744;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human apolipoprotein-like ORF717 protein, SEQ ID NO:1434.
XX
KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; neurotropic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide.
XX
OS Homo sapiens.
XX
XX WO200190366-A2.
PN
XX
PD 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US017076.
PF
XX
XX 24-MAY-2000; 2000US-0206690P.

XX (CURA-) CURAGEN CORP.
XX PA
XX PI
XX Leach MD, Shinkets RA;
XX WPI; 2002-106200/14.
DR N-PSDB; ABN75770.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation.
XX
PS Claim 10; Page 625; 2508pp; English.
XX
CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN79587 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases
XX
SQ Sequence 64 AA;

Query Match 18.3%; Score 162; DB 5; Length 64;
Best local similarity 75.0%; Pred. No. 4.2e-06;
Matches 30; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ 41
: ||| ||||| ||||| : ||||| : ||||| ||||| : |||
Db 25 DEPQSQWDRVKDFATVYVDVAVKDSGRNYVSQFESSTLGQQ 64

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OM protein - protein search, using sw model

Run on: December 21, 2004, 13:22:55 ; Search time 144 Seconds
(without alignments)
422.444 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_194
Perfect score: 885
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....RARAHVDA LRTHLAPYSDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 921198

Minimum DB seq length: 0
Maximum DB seq length: 170

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|----------------------|
| 1 | 885 | 100.0 | 170 | 9 | US-09-803-918A-3 |
| 2 | 647.5 | 73.2 | 166 | 14 | US-10-291-172-729 |
| 3 | 647.5 | 73.2 | 166 | 15 | US-10-221-278-729 |
| 4 | 529.5 | 59.8 | 168 | 15 | US-10-465-789A-29 |
| 5 | 529.5 | 59.8 | 168 | 15 | US-10-465-789A-82 |
| 6 | 451.5 | 51.0 | 93 | 15 | US-10-038-854-403 |
| 7 | 451.5 | 51.0 | 93 | 15 | US-10-038-854-405 |
| 8 | 442.5 | 50.0 | 168 | 15 | US-10-465-789A-23 |
| 9 | 437 | 49.4 | 158 | 16 | US-10-408-765A-2201 |
| 10 | 396.5 | 44.8 | 168 | 15 | US-10-465-789A-81 |
| 11 | 318 | 35.9 | 86 | 15 | US-10-424-599-276814 |
| 12 | 227 | 25.6 | 43 | 15 | US-10-465-789A-89 |
| 13 | 162 | 18.3 | 64 | 11 | US-09-864-408A-1434 |

| | | | | | | |
|----|-------|------|-----|----|----------------------|-------------------|
| 14 | 137 | 15.5 | 26 | 14 | US-10-120-508-21 | Sequence 21, Appl |
| 15 | 122 | 13.8 | 22 | 15 | US-10-465-789A-52 | Sequence 52, Appl |
| 16 | 118 | 13.3 | 22 | 15 | US-10-465-789A-50 | Sequence 50, Appl |
| 17 | 113 | 12.8 | 22 | 15 | US-10-465-789A-54 | Sequence 54, Appl |
| 18 | 112 | 12.7 | 22 | 15 | US-10-465-789A-49 | Sequence 49, Appl |
| 19 | 108 | 12.2 | 22 | 15 | US-10-465-789A-53 | Sequence 53, Appl |
| 20 | 106.5 | 12.0 | 107 | 14 | US-10-023-066A-92 | Sequence 92, Appl |
| 21 | 96.5 | 10.9 | 95 | 17 | US-10-487-096-2 | Sequence 2, Appli |
| 22 | 94 | 10.6 | 18 | 14 | US-10-142-238A-10 | Sequence 10, Appl |
| 23 | 94 | 10.6 | 30 | 14 | US-10-142-238A-40 | Sequence 40, Appl |
| 24 | 94 | 10.6 | 30 | 14 | US-10-142-238A-41 | Sequence 41, Appl |
| 25 | 92 | 10.4 | 18 | 14 | US-10-142-238A-33 | Sequence 33, Appl |
| 26 | 91 | 10.3 | 158 | 15 | US-10-424-599-198597 | Sequence 198597, |
| 27 | 90 | 10.2 | 18 | 14 | US-10-142-238A-13 | Sequence 13, Appl |
| 28 | 90 | 10.2 | 160 | 9 | US-09-764-864-1129 | Sequence 1129, Ap |
| 29 | 90 | 10.2 | 162 | 17 | US-10-425-115-186898 | Sequence 186898, |
| 30 | 89 | 10.1 | 16 | 17 | US-10-700-340-37 | Sequence 37, Appl |
| 31 | 89 | 10.1 | 30 | 14 | US-10-142-238A-39 | Sequence 39, Appl |
| 32 | 89 | 10.1 | 30 | 14 | US-10-142-238A-43 | Sequence 43, Appl |
| 33 | 88 | 9.9 | 129 | 10 | US-09-769-787-51 | Sequence 51, Appl |
| 34 | 87 | 9.8 | 17 | 15 | US-10-601-100-44 | Sequence 44, Appl |
| 35 | 87 | 9.8 | 18 | 14 | US-10-142-238A-32 | Sequence 32, Appl |
| 36 | 87 | 9.8 | 18 | 14 | US-10-142-238A-35 | Sequence 35, Appl |
| 37 | 87 | 9.8 | 89 | 17 | US-10-425-115-191061 | Sequence 191061, |
| 38 | 86 | 9.7 | 18 | 14 | US-10-142-238A-9 | Sequence 9, Appli |
| 39 | 86 | 9.7 | 18 | 14 | US-10-142-238A-11 | Sequence 11, Appl |
| 40 | 86 | 9.7 | 18 | 14 | US-10-142-238A-14 | Sequence 14, Appl |
| 41 | 86 | 9.7 | 30 | 14 | US-10-142-238A-42 | Sequence 42, Appl |
| 42 | 86 | 9.7 | 30 | 14 | US-10-142-238A-46 | Sequence 46, Appl |
| 43 | 85.5 | 9.7 | 109 | 14 | US-10-029-386-29332 | Sequence 29332, A |
| 44 | 85.5 | 9.7 | 165 | 16 | US-10-767-701-42732 | Sequence 42732, A |
| 45 | 85 | 9.6 | 18 | 14 | US-10-142-238A-12 | Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-09-803-918A-3
; Sequence 3, Application US/09803918A
; Patent No. US20020064820A1
; GENERAL INFORMATION:
; APPLICANT: Dayer, Jean-Michel
; APPLICANT: Burger, Danielle
; APPLICANT: Kohno, Tadahiko
; APPLICANT: Edwards III, Carl K.
; TITLE OF INVENTION: APO-A-1 REGULATION OF T-CELL SIGNALING
; FILE REFERENCE: 06843.0035-00000
; CURRENT APPLICATION NUMBER: US/09/803,918A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/189,008
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/193,551
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(170)
; OTHER INFORMATION: 18 kDa N-terminal fragment
US-09-803-918A-3

Query Match 100.0%; Score 885; DB 9; Length 170;
Best Local Similarity 100.0%; Pred.No. 1.9e-64;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLDNWDSVTSTFSKL 60
|||||
Db 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLDNWDSVTSTFSKL 60

[illegible]

```

RESULT 2
US-10-291-172-729
; Sequence 729, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 729
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-729

```

| | | | | |
|---------------------------|--------|--------------------|------------|-------------|
| Query Match | 73.2%; | Score 647.5; | DB 14; | Length 166; |
| Best Local Similarity | 82.7%; | Pred. No. 4.4e-45; | | |
| Matches 129; Conservative | 1; | Mismatches 3; | Indels 23; | Gaps 1 |

| | | | |
|----|-----|---|-----|
| QY | 1 | DEPPQPWDRVKOLATVYVDVLKDSGRDYVSQFEKSALGQLNLKLNDWDSVTSTFSKL | 60 |
| | | : | |
| Dd | 34 | DEPPQPWDRVKOLATVYVDVLKDSGK-----DSVTSTFSKL | 70 |
| | | | |
| QY | 61 | REQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVEKAKVPYLDDFQKKQEEMELYRQKVE | 120 |
| | | | |
| Dd | 71 | REQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVEKAKVPYLDDFQKKQEEMELYRQKVE | 130 |
| | | | |
| QY | 121 | PLRAELOEGARQKLHELQEKLSPLGEEMRDRAHV | 156 |
| | | | |
| Dd | 131 | PLRAELOEGARQKLHELQEKLSPLGEEDADRRRAHV | 166 |

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; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 729
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-729

Query Match          73.2%; Score 647.5; DB 15; Length 166;
Best Local Similarity 82.7%; Pred.No. 4.4e-45;
Matches 129; Conservative 1; Mismatches 3; Indels 23; Gaps 1;

QY   1 DEPPQSPWDRVKDLATVVDVLKDSGRDYSVFEGSALGKQLNLKLLDNWDSDVTSTFSKL 60
      |||||
Db    34 DEPPQSPWDRVKDLATVVDVLKDSGK-----DSVTSTFSKL 70

QY   61 REQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVPYLDLDFKKWEEMELYRQKVE 120
      |||||
Db    71 REQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVPYLDLDFKKWEEMELYRQKVE 130

QY   121 PLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV 156
       |||||
Db    131 PLRAELQEGARQKLHELQEKLSPLGEEDADRRRAHV 166


RESULT 4
US-10-465-789A-29
; Sequence 29, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His-tagged MSPID6
US-10-465-789A-29

Query Match          59.8%; Score 529.5; DB 15; Length 168;
Best Local Similarity 74.5%; Pred.No. 1.9e-35;
Matches 108; Conservative 5; Mismatches 25; Indels 7; Gaps 1;

QY   26 GRDYVSQFEGSALGKQLNLKLLDNWDSDVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE 85
      | : ||
Db    2 GHHHHHHIEG-----RLKLLDNWDSDVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE 54

QY   86 MSKDLEEVKAKVPYLDLDFKKWEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
      |||||
Db    55 MSKDLEEVKAKVPYLDLDFKKWEEMELYRQKVEPLRAELQEGARQKLHELQEKLSARL 114

QY   146 EEMRDRARAHDVALRTHLAPYSDEL 170
      | : | | | | | : | |
Db    115 AEYHAKATEHLSTLSEKAKPALEDL 139

```



```
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 405
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-854-405

Query Match          51.0%; Score 451.5; DB 15; Length 93;
Best Local Similarity 77.5%; Pred. No. 2.1e-29;
Matches 93; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 14 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 73
      |||||
Db 1 LATVYVDVLK-----DSVTSTFSKLREQLGPVTQEFWD 33

QY 74 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQK 133
      |||||
Db 34 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQK 93

RESULT 8
US-10-465-789A-23
; Sequence 23, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
```

```
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His-tagged MSP1D5D6
; US-10-465-789A-23

Query Match          50.0%; Score 442.5; DB 15; Length 168;
Best Local Similarity 63.4%; Pred. No. 2.4e-28;
Matches 92; Conservative 9; Mismatches 37; Indels 7; Gaps 1;

QY 26 GRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE 85
      | : ||
Db 2 GHHHHHHIEG-----RLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE 54

QY 86 MSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
      |||||
Db 55 MSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPYSDELRLQRLAARLEALKENGCGARL 114

QY 146 EEMRDRARAHVDALRTHLAPYSDEL 170
      | : || : |
Db 115 AETHAKATEHLSTLSEKAKPALEDL 139

RESULT 9
US-10-408-765A-2201
; Sequence 2201, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2201
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-2201

Query Match          49.4%; Score 437; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.2e-28;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 MSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
      |||||
Db 1 MSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 60

QY 146 EEMRDRARAHVDALRTHLAPYSDEL 170
      |||||
Db 61 EEMRDRARAHVDALRTHLAPYSDEL 85

RESULT 10
US-10-465-789A-81
; Sequence 81, Application US/10465789A
; Publication No. US20040053384A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of MSP1D4D5
US-10-465-789A-81

Query Match          44.8%; Score 396.5; DB 15; Length 168;
Best Local Similarity 65.4%; Pred. No. 1.4e-24;
Matches 83; Conservative 0; Mismatches 0; Indels 44; Gaps 1;

QY 44 LKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDD 103
Db 13 LKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQ----- 67

QY 104 FQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHL 163
Db 68 -----PLGEEMRDRARAHVDALRTHL 88

QY 164 APYSDEL 170
Db 89 APYSDEL 95

RESULT 11
US-10-424-599-276814
; Sequence 276814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276814
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91983C.1.pap
US-10-424-599-276814

Query Match          35.9%; Score 318; DB 15; Length 86;
Best Local Similarity 98.4%; Pred. No. 1.5e-18;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60
Db 25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVDSTFSKL 84
```

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QY 61 RE 62
Db 85 RE 86

RESULT 12
US-10-465-789A-89
; Sequence 89, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of GLOB
US-10-465-789A-89

Query Match          25.6%; Score 227; DB 15; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLN 43
Db 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLN 43

RESULT 13
US-09-864-408A-1434
; Sequence 1434, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Enc
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1434
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-864-408A-1434

Query Match          18.3%; Score 162; DB 11; Length 64;
Best Local Similarity 75.0%; Pred. No. 5.7e-06;
Matches 30; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ 41
Db 25 DEPPQSPWDRVKDFATVYVDVAVKDSGRNYVSQFESSTLQQ 64
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RESULT 14

US-10-120-508-21
; Sequence 21, Application US/10120508
; Publication No. US20030191057A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: G-TYPE PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-301100US
; CURRENT APPLICATION NUMBER: US/10/120,508
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic D peptide.
US-10-120-508-21

Query Match 15.5%; Score 137; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 WDRVKDLATVYVDVLKDSGRDYVSQF 33
|||
Db 1 WDRVKDLATVYVDVLKDSGRDYVSQF 26

RESULT 15

US-10-465-789A-52
; Sequence 52, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 4
US-10-465-789A-52

Query Match 13.8%; Score 122; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 PYLDDFQKKQEEEMELYRQKVE 120
|||
Db 1 PYLDDFQKKQEEEMELYRQKVE 22

Search completed: December 21, 2004, 13:39:57
Job time : 145 secs

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OM protein - protein search, using sw model

Run on: December 21, 2004, 13:37:37 ; Search time 39 Seconds
(without alignments)
289.078 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_194
Perfect score: 885
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....RARAHVDA LRTHLAPYSDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 358685

Minimum DB seq length: 0
Maximum DB seq length: 170

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|--|
| 1 | 328 | 37.1 | 64 | 2 | US-08-292-870-1 Sequence 1, Appli |
| 2 | 227 | 25.6 | 44 | 2 | US-08-292-870-2 Sequence 2, Appli |
| 3 | 163 | 18.4 | 32 | 2 | US-08-292-870-3 Sequence 3, Appli |
| 4 | 124 | 14.0 | 25 | 2 | US-08-292-870-4 Sequence 4, Appli |
| 5 | 106.5 | 12.0 | 107 | 1 | US-08-182-175A-105 Sequence 105, App |
| 6 | 106.5 | 12.0 | 107 | 1 | US-08-474-633A-92 Sequence 92, Appl |
| 7 | 106.5 | 12.0 | 107 | 4 | US-08-823-771-92 Sequence 92, Appl |
| 8 | 106.5 | 12.0 | 107 | 5 | PCT-US92-06412-105 Sequence 105, App |
| 9 | 101 | 11.4 | 128 | 4 | US-09-621-976-5220 Sequence 5220, Ap |
| 10 | 100 | 11.3 | 110 | 1 | US-07-849-389-7 Sequence 7, Appli |
| 11 | 91 | 10.3 | 16 | 1 | US-07-959-946-5 Sequence 5, Appli |
| 12 | 91 | 10.3 | 16 | 1 | US-08-333-577-5 Sequence 5, Appli |
| 13 | 91 | 10.3 | 16 | 5 | PCT-US92-08634-5 Sequence 5, Appli |
| 14 | 89 | 10.1 | 114 | 4 | US-09-079-030-129 Sequence 129, App |
| 15 | 88 | 9.9 | 129 | 4 | US-09-583-110-3496 Sequence 3496, Ap |
| 16 | 84.5 | 9.5 | 105 | 2 | US-08-743-200-2 Sequence 2, Appli |
| 17 | 81.5 | 9.2 | 131 | 4 | US-09-513-999C-5882 Sequence 5882, Ap |
| 18 | 81 | 9.2 | 103 | 4 | US-09-134-000C-4548 Sequence 4548, Ap |
| 19 | 81 | 9.2 | 147 | 4 | US-08-529-055-18 Sequence 18, Appl |
| 20 | 81 | 9.2 | 153 | 4 | US-08-529-055-23 Sequence 23, Appl |
| 21 | 81 | 9.2 | 156 | 4 | US-09-270-767-32734 Sequence 32734, A |
| 22 | 81 | 9.2 | 156 | 4 | US-09-270-767-47951 Sequence 47951, A |
| 23 | 81 | 9.2 | 160 | 4 | US-08-529-055-33 Sequence 33, Appl |
| 24 | 80.5 | 9.1 | 159 | 4 | US-09-248-796A-16325 Sequence 16325, A |
| 25 | 80 | 9.0 | 72 | 1 | US-08-182-175A-87 Sequence 87, Appl |
| 26 | 80 | 9.0 | 72 | 5 | PCT-US92-06412-87 Sequence 87, Appl |
| 27 | 78 | 8.8 | 166 | 1 | US-08-365-103B-14 Sequence 14, Appl |

| | | | | | |
|----|------|-----|-----|---|--|
| 28 | 78 | 8.8 | 167 | 1 | US-08-365-103B-12 Sequence 12, Appl |
| 29 | 77.5 | 8.8 | 144 | 4 | US-09-270-767-62028 Sequence 62028, A |
| 30 | 77.5 | 8.8 | 164 | 4 | US-09-270-767-59203 Sequence 59203, A |
| 31 | 76.5 | 8.6 | 114 | 4 | US-09-513-999C-6218 Sequence 6218, Ap |
| 32 | 76 | 8.6 | 96 | 4 | US-09-513-999C-5524 Sequence 5524, Ap |
| 33 | 76 | 8.6 | 114 | 4 | US-09-252-991A-18411 Sequence 18411, A |
| 34 | 76 | 8.6 | 137 | 4 | US-09-513-999C-7081 Sequence 7081, Ap |
| 35 | 74.5 | 8.4 | 105 | 4 | US-09-513-999C-6681 Sequence 6681, Ap |
| 36 | 74.5 | 8.4 | 157 | 4 | US-09-270-767-41567 Sequence 41567, A |
| 37 | 73.5 | 8.3 | 99 | 4 | US-09-270-767-44037 Sequence 44037, A |
| 38 | 73 | 8.2 | 144 | 4 | US-09-270-767-34931 Sequence 34931, A |
| 39 | 73 | 8.2 | 144 | 4 | US-09-270-767-50148 Sequence 50148, A |
| 40 | 73 | 8.2 | 145 | 2 | US-08-686-599A-20 Sequence 20, Appl |
| 41 | 73 | 8.2 | 153 | 4 | US-09-134-000C-5741 Sequence 5741, Ap |
| 42 | 73 | 8.2 | 165 | 4 | US-09-898-554-24 Sequence 24, Appl |
| 43 | 73 | 8.2 | 166 | 4 | US-09-270-767-59533 Sequence 59533, A |
| 44 | 72 | 8.1 | 124 | 4 | US-09-270-767-45785 Sequence 45785, A |
| 45 | 71.5 | 8.1 | 108 | 2 | US-08-710-749-24 Sequence 24, Appl |

ALIGNMENTS

RESULT 1
US-08-292-870-1
; Sequence 1, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-1

Query Match      37.1%; Score 328; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 EMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPL 144
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Db 1 EMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPL 60

QY 145 GEEM 148
    ||||
Db 61 GEEM 64

RESULT 2
US-08-292-870-2
; Sequence 2, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-2
Query Match      18.4%; Score 163; DB 2; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.9e-08;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Query Match      25.6%; Score 227; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 ROEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAEL 126
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Db 1 ROEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAEL 44

RESULT 3
US-08-292-870-3
; Sequence 3, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa can be either E (Glu)
; OTHER INFORMATION: or F (Phe)"
US-08-292-870-3
Query Match      18.4%; Score 163; DB 2; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.9e-08;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-633A-92

Query Match 12.0%; Score 106.5; DB 1; Length 107;
Best Local Similarity 27.3%; Pred. No. 0.02;
Matches 27; Conservative 28; Mismatches 35; Indels 9; Gaps 3;

QY 59 KLRQLGPVTQEFW-----DNLEKETEGLRQEMSKOLEEVKA--KVQPYLDDFQKKWQE 110
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Db 7 KLKEEMAKMKDEMWKLEEMKKLEEMKVMEEKMKKLEEMKAMEDKMKWLEEKMKKLEE 66

QY 111 EMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMR 149
:|::: :| : | : | :| :| :| :| :| :| :| :| :| :| :| :|
Db 67 KMKVMEEMKKLE-EKMKAMEDKMKWLEEKMKKLEEMK 104

RESULT 7
US-08-823-771-92
; Sequence 92, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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;
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-08-823-771-92

Query Match 12.0%; Score 106.5; DB 4; Length 107;
Best Local Similarity 27.3%; Pred. No. 0.02;
Matches 27; Conservative 28; Mismatches 35; Indels 9; Gaps 3;

QY 59 KLRQLGPVTQEFW-----DNLEKETEGLRQEMSKOLEEVKA--KVQPYLDDFQKKWQE 110
||::: : | | ||::: : : | | ||::: : : | | ||::: : : | |
Db 7 KLKEEMAKMKDEMWKLEEMKKLEEMKVMEEKMKKLEEMKAMEDKMKWLEEKMKKLEE 66

QY 111 EMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMR 149
:|::: :| : | : | :| :| :| :| :| :| :| :| :| :| :| :|
Db 67 KMKVMEEMKKLE-EKMKAMEDKMKWLEEKMKKLEEMK 104

RESULT 8
PCT-US92-06412-105
; Sequence 105, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-06412-105
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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-959-946-5

Query Match 10.3%; Score 91; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 KVQPYLDDFQKKWQEE 111
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Db 1 KVQPYLDDFQKKWQEE 16

RESULT 12
US-08-333-577-5
; Sequence 5, Application US/08333577
; Patent No. 5786206
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,577
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 234.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-333-577-5

Query Match 10.3%; Score 91; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 KVQPYLDDFQKKWQEE 111
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Db 1 KVQPYLDDFQKKWQEE 16

RESULT 13
PCT-US92-08634-5

; Sequence 5, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08634
; FILING DATE: 19921009
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-08634-5

Query Match 10.3%; Score 91; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 KVQPYLDDFQKKWQEE 111
| | | | | | | | | | | | | | | |
Db 1 KVQPYLDDFQKKWQEE 16

RESULT 14
US-09-079-030-129
; Sequence 129, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.
; APPLICANT: Hoogveen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 13:19:15 ; Search time 38 Seconds
(without alignments)
303.842 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_144
 Perfect score: 631
 Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LDDFQKQWEEMLYRKVE 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 52135

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Minimum DB seq length: 0
Maximum DB seq length: 120
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :      PIR 79:*
1:  _pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 106 | 16.8 | 34 | 2 | S67972 | apolipoprotein AI |
| 2 | 106 | 16.8 | 36 | 2 | A56866 | apolipoprotein A-I |
| 3 | 101 | 16.0 | 20 | 2 | A05313 | apolipoprotein A-I |
| 4 | 81 | 12.8 | 118 | 2 | B69818 | conserved hypothetical |
| 5 | 76.5 | 12.1 | 79 | 2 | G86722 | hypothetical protein |
| 6 | 76 | 12.0 | 99 | 2 | B46598 | ski-related protein |
| 7 | 69 | 10.9 | 79 | 2 | S53443 | kinetoplastid memb |
| 8 | 66 | 10.5 | 113 | 2 | C89923 | hypothetical protein |
| 9 | 65.5 | 10.4 | 92 | 2 | S53442 | kinetoplastid memb |
| 10 | 65 | 10.3 | 113 | 2 | I40399 | flagellar protein |
| 11 | 64.5 | 10.2 | 104 | 2 | A60094 | neurofilament-M ho |
| 12 | 64.5 | 10.2 | 115 | 2 | C86901 | hypothetical protein |
| 13 | 63.5 | 10.1 | 109 | 2 | F71511 | hypothetical protein |
| 14 | 63 | 10.0 | 107 | 1 | H64112 | virulence-associated |
| 15 | 62 | 9.8 | 106 | 2 | C90261 | hypothetical protein |
| 16 | 61.5 | 9.7 | 96 | 2 | I68742 | integral membrane |
| 17 | 61.5 | 9.7 | 119 | 2 | B82904 | hypothetical protein |
| 18 | 61 | 9.7 | 75 | 2 | C90225 | hypothetical protein |
| 19 | 61 | 9.7 | 75 | 2 | C90342 | hypothetical protein |
| 20 | 61 | 9.7 | 108 | 2 | A59010 | antifreeze protein |
| 21 | 60.5 | 9.6 | 73 | 2 | H81298 | probable molybdopt |
| 22 | 60.5 | 9.6 | 107 | 2 | D95153 | hypothetical protein |
| 23 | 60 | 9.5 | 113 | 2 | H97483 | hypothetical protein |
| 24 | 60 | 9.5 | 119 | 2 | D75111 | hypothetical protein |
| 25 | 60 | 9.5 | 119 | 2 | E70049 | hypothetical protein |
| 26 | 59.5 | 9.4 | 76 | 2 | D82445 | hypothetical protein |
| 27 | 59.5 | 9.4 | 99 | 2 | JU0038 | nonhistone chromos |
| 28 | 59.5 | 9.4 | 109 | 2 | F81669 | conserved hypothetical |
| 29 | 59.5 | 9.4 | 117 | 2 | H71978 | hypothetical protein |

| | | | | | | |
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| 30 | 59.5 | 9.4 | 120 | 2 | AB1425 | hypothetical prote |
| 31 | 59 | 9.4 | 79 | 2 | AE0012 | conserved hypothet |
| 32 | 59 | 9.4 | 102 | 2 | D97844 | hypothetical prote |
| 33 | 58.5 | 9.3 | 76 | 2 | JC5734 | apolipoprotein A-I |
| 34 | 58.5 | 9.3 | 79 | 2 | AB3643 | hypothetical cytos |
| 35 | 58.5 | 9.3 | 85 | 2 | C65120 | hypothetical 10.0 |
| 36 | 58.5 | 9.3 | 93 | 2 | AF3532 | transposase BME110 |
| 37 | 58.5 | 9.3 | 93 | 2 | AI3537 | transposase BME110 |
| 38 | 58.5 | 9.3 | 111 | 2 | B90187 | hypothetical prote |
| 39 | 58.5 | 9.3 | 120 | 2 | AD1468 | ribosomal protein |
| 40 | 58 | 9.2 | 71 | 2 | A69154 | conserved hypothet |
| 41 | 58 | 9.2 | 88 | 2 | A72222 | hypothetical prote |
| 42 | 58 | 9.2 | 103 | 2 | B69466 | hypothetical prote |
| 43 | 58 | 9.2 | 105 | 2 | C83942 | hypothetical prote |
| 44 | 58 | 9.2 | 109 | 2 | E34510 | homeotic protein E |
| 45 | 58 | 9.2 | 110 | 2 | E70157 | conserved hypothet |

ALIGNMENTS

RESULT 1

S67972
 apolipoprotein AI - goose (fragment)
 C:Species: Anser anser (domestic goose)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S67972
 R:Hermier, D.; Sellier, N.; Rousselot-Pailley, D.; Forgez, P.
 Eur. J. Biochem. 234, 586-591, 1995
 A:Title: Characterization of apolipoproteins B-100, AI and C from plasma li
 A:Reference number: S67972; MUID:96128192; PMID:8536707

```
Query Match      16.8%; Score 106; DB 2; Length 34;
Best Local Similarity 54.5%; Pred. No. 0.03;
Matches 18; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
```

[illegible]

RESULT 2

A56866
apolipoprotein A-I - Japanese quail (fragment)
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56866
R:Oku, H.; Ishikawa, M.; Nagata, J.; Toda, T.; Chinen, I.
Biochim. Biophys. Acta 1167, 22-28, 1993
A:Title: Lipoprotein and apoprotein profile of Japanese quail.
A:Reference number: A56866; MUID:93213845; PMID:8461329
A:Accession: A56866
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-36 <OKU>
A:Cross-references: UNIPROT:P32918
A:Note: sequence extracted from NCBI backbone (NCBIP:128831)
A:Note: this protein was found primarily as a 26K apoprotein
C:Superfamily: apolipoprotein A-I

```
Query Match      16.8%; Score 106; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.032;
Matches 18: Conservative 10; Mismatches 8; Indels 0; Gaps 0;
```

QY 2 EPQPSPWDRVKDLATVYVDVLKDSGRDYVSQFESSA 37
 : |||: |||::|: ||::: |||: |:|||: ||
Dp 1 DPOTPLDIRIDMLDPLYETKVASGKOAISOFESSA 36

| | | | | |
|-----------------------|--------|--------------------|-------|-----------------------------------|
| Query Match | 10.2%; | Score 64.5; | DB 2; | Length 104; |
| Best Local Similarity | 24.0%; | Pred. No. 1.8e+02; | | |
| Matches | 24; | Conservative | 18; | Mismatches 35; Indels 23; Gaps 4; |

| | | | |
|----|----|---|----|
| QY | 25 | SGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVT-----QEFWDN | 74 |
| Db | 15 | SAKDEIAEYR-----RQIHSKTVE-LESVGRGTESLERQLNDIERHGHDLTSYQETIQQ | 68 |

| | | | |
|----|----|--|-----|
| QY | 75 | LEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMEL | 114 |
| Db | 69 | LDNELRGTKWEMSRHLRE-----YQDLLNVKMAIDIEI | 101 |

RESULT 12

C86901

hypothetical protein ywjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C;Accession: C86901

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Mialarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: C86901

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-115 <STO>

A;Cross-references: UNIPROT:Q9CDK8; GB:AE005176; PID:g12725277; PIDN:AAK06309.1; GSPDB:G

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: ywjB

| | | | | |
|-----------------------|--------|------------------|-------|-----------------------------------|
| Query Match | 10.2%; | Score 64.5; | DB 2; | Length 115; |
| Best Local Similarity | 20.2%; | Pred. No. 2e+02; | | |
| Matches | 21; | Conservative | 24; | Mismatches 44; Indels 15; Gaps 3; |

| | | | |
|----|----|--|----|
| QY | 13 | DLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQE-- | 70 |
| Db | 5 | DLVDLLVEKIK--SLDYVKDFQQAETALMANQELF-----KAQEMKALQKEAV | 51 |

| | | | |
|----|----|--|-----|
| QY | 71 | FWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMEL | 114 |
| Db | 52 | LYQKIDKMQAYKKTSSQAQVIEKRIKLHPLVEDYATKLEDVNDL | 95 |

RESULT 13

F71511

hypothetical protein CT466 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C;Species: Chlamydia trachomatis

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: F71511

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia

A;Reference number: A71570; MUID:99000809; PMID:9784136

A;Accession: F71511

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-109 <ARN>

A;Cross-references: UNIPROT:O84472; GB:AE001320; GB:AE001273; NID:g3328891; PIDN:AAAC6806

A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:

A;Gene: CT466

C;Superfamily: conserved hypothetical protein CP0165

| | | | | |
|-----------------------|--------|--------------------|-------|-----------------------------------|
| Query Match | 10.1%; | Score 63.5; | DB 2; | Length 109; |
| Best Local Similarity | 24.7%; | Pred. No. 2.3e+02; | | |
| Matches | 22; | Conservative | 25; | Mismatches 31; Indels 11; Gaps 4; |

| | | | |
|----|----|---|----|
| QY | 30 | VSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKD | 89 |
| Db | 23 | LTQVEASLSPEDL-IKVLROKKTLLSCIEKVDHQI-----KKFRDSF---SLALPQEVQEE | 74 |

Qy 90 LEEVKAKVQPYLDDFQKKW---QEEMELY 115
|||:::| |: |: |: |: |: |
Db 75 LEEIRSVIQRILETDKKNYCIRKRELRTY 103

RESULT 14
H64112
virulence-associated protein vapA homolog H11251 - Haemophilus influenzae (strain Rd KW2)
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H64112
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64112
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <TIGR>
A;Cross-references: UNIPROT:Q57089; GB:U32805; GB:L42023; NID:g1574180; PIDN:AAC22901.1;
C;Superfamily: virulence-associated protein vapA
C;Keywords: DNA binding; transcription regulation

Query Match 10.0%; Score 63; DB 1; Length 107;
Best Local Similarity 23.9%; Pred. No. 2.4e+02;
Matches 22; Conservative 21; Mismatches 31; Indels 18; Gaps 3;
Qy 10 RVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQ 69
:: |||:::| |: |: |: |: |: |
Db 24 KISDLAQI-LDVHRNTASNIVN--NSSRITLEMAVKLAKVFDT-----TP 65
Qy 70 EFWDNLEKETEGLRQEMSKDLEEVKAKVQPYL 101
||| |||:::| |: |: |: |: |: |
Db 66 EFWLNLTQTRIDLWDLEHNKRFFQQSLANVKPAL 97

RESULT 15
C90261
hypothetical protein SSO1086 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90261
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90261
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <KUR>
A;Cross-references: UNIPROT:Q97Z50; GB:AE006641; NID:g13814276; PIDN:AAK41346.1; GSPDB:G
C;Genetics:
A;Gene: SSO1086

Query Match 9.8%; Score 62; DB 2; Length 106;
Best Local Similarity 32.5%; Pred. No. 2.9e+02;
Matches 25; Conservative 15; Mismatches 21; Indels 16; Gaps 5;
Qy 48 DNWDSVTS-----TFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQP 99
: || |||:::| |: |: |: |: |: |
Db 35 NNWVSVSAERFSRNDPSINKVKEAVKYATHE--EDLKAIEELRSSGIK-IEEVKE--IP 89
Qy 100 YLDDF---QKKWQEEME 113
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Search completed: December 21, 2004, 13:31:26
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 13:19:55 ; Search time 190 Seconds
(without alignments) 363.395 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_144
Perfect score: 631
Sequence: 1 DEPPQSPWDRVKDLATVVD.....LDDFKKQWEEMLYRQKVE 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 393250

```
Minimum DB seq length: 0
Maximum DB seq length: 120
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|------------|-------|-------|--------|----|------------|---------------------|
| | | Match | Length | | | |
| 1 | 247 | 39.1 | 56 | 2 | O02762 | O02762 ovis aries |
| 2 | 226 | 35.8 | 79 | 2 | Q6LD50 | Q6LD50 mus sp. apo |
| 3 | 226 | 35.8 | 79 | 2 | AAB35539 | AAB35539 mus sp. a |
| 4 | 217 | 34.4 | 82 | 2 | Q29248 | Q29248 sus scrofa |
| 5 | 141 | 22.3 | 26 | 2 | Q9UCT8 | Q9uct8 homo sapien |
| 6 | 106 | 16.8 | 34 | 2 | Q9PRR6 | Q9prrr6 anser anser |
| 7 | 101 | 16.0 | 20 | 1 | APAL_ERYPA | P18647 erythrocebu |
| 8 | 101 | 16.0 | 30 | 2 | Q9QV04 | Q9qv04 rattus sp. |
| 9 | 85 | 13.5 | 107 | 1 | APE_MACMU | Q28502 macaca mula |
| 10 | 83 | 13.2 | 107 | 1 | APE_SAISC | Q28995 saimiri sci |
| 11 | 81 | 12.8 | 118 | 2 | O07516 | O07516 bacillus su |
| 12 | 77.5 | 12.3 | 96 | 2 | Q7P280 | Q7p280 fusobacteri |
| 13 | 76.5 | 12.1 | 79 | 2 | Q9CHE9 | Q9che9 lactococcus |
| 14 | 76 | 12.0 | 99 | 2 | Q9PSS3 | Q9pss3 gallus gall |
| 15 | 76 | 12.0 | 118 | 2 | O68959 | O68959 streptococc |
| 16 | 75 | 11.9 | 117 | 2 | O68958 | O68958 streptococc |
| 17 | 74.5 | 11.8 | 102 | 2 | Q9XPX4 | Q9pxp4 hepatitis c |
| 18 | 73 | 11.6 | 76 | 2 | Q6WHJ6 | Q6whj6 bacterioph |
| 19 | 73 | 11.6 | 76 | 2 | AAQ64377 | Aaq64377 bacteriop |
| 20 | 73 | 11.6 | 93 | 2 | Q81R54 | Q81r54 bacillus an |
| 21 | 73 | 11.6 | 93 | 2 | AAT31321 | Aat31321 bacillus |
| 22 | 73 | 11.6 | 113 | 2 | Q8IIF8 | Q8iif8 plasmodium |
| 23 | 72 | 11.4 | 92 | 2 | Q7YZC6 | Q7yzc6 trypanosoma |
| 24 | 72 | 11.4 | 102 | 2 | Q29258 | Q29258 sus scrofa |
| 25 | 70.5 | 11.2 | 92 | 2 | Q9GU60 | Q9gu60 leishmania |
| 26 | 70.5 | 11.2 | 114 | 2 | Q9ZFZ1 | Q9zffz1 streptococc |
| 27 | 70 | 11.1 | 92 | 1 | KM11_TRYBB | Q26773 trypanosoma |
| 28 | 70 | 11.1 | 92 | 2 | Q7YZC5 | Q7yzc5 trypanosoma |
| 29 | 69.5 | 11.0 | 92 | 2 | Q9XZH5 | Q9xzh5 leishmania |
| 30 | 69 | 10.9 | 104 | 2 | Q54892 | Q54892 streptococc |
| 31 | 68 | 10.8 | 90 | 2 | Q9LCR0 | Q9lcr0 paenibacilli |

| Accession | Gene | Length (bp) | GC (%) | Accession | Gene | Length (bp) | GC (%) |
|-----------|-------------|-------------|--------|-----------|------------|-------------|--------|
| Q6bmu6 | debariomyce | 68 | 10.8 | 2 | Q6BMU6 | 101 | 10.8 |
| O85812 | streptococc | 68 | 10.8 | 2 | O85812 | 105 | 10.8 |
| O43974 | leishmania | 67.5 | 10.7 | 92 | O43974 | 92 | 10.7 |
| Q9rhf1 | streptococc | 67 | 10.6 | 78 | Q9RHF1 | 78 | 10.6 |
| Q8is88 | trypanosoma | 67 | 10.6 | 92 | Q8IS88 | 92 | 10.6 |
| P89597 | human immun | 67 | 10.6 | 95 | P89597 | 95 | 10.6 |
| Q25297 | leishmania | 66.5 | 10.5 | 92 | K11B_LEIIN | 92 | 10.5 |
| Q25298 | leishmania | 66.5 | 10.5 | 1 | K11C_LEIIN | 92 | 10.5 |
| Q21436 | leishmania | 66.5 | 10.5 | 92 | KM11_LEITR | 92 | 10.5 |
| Q6rv15 | leishmania | 66.5 | 10.5 | 92 | Q6RV15 | 92 | 10.5 |
| Aar84616 | leishmani | 66.5 | 10.5 | 92 | AAR84616 | 92 | 10.5 |
| Q6nk47 | corynebacte | 66 | 10.5 | 80 | Q6NK47 | 80 | 10.5 |
| Cae48695 | corynebact | 66 | 10.5 | 80 | CAE48695 | 80 | 10.5 |
| Q36736 | leishmania | 66 | 10.5 | 92 | KM11_LEIDO | 92 | 10.5 |

ALIGNMENTS

```

RESULT 1
002762
ID      002762      PRELIMINARY;      PRT;      56 AA.
AC      002762;
DT      01-JUL-1997 (TrEMBLrel. 04, Created)
DT      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Apolipoprotein A1 (Fragment).
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Caprinae; Ovis.
OX      NCBI_TaxID=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99098454; PubMed=9883985;
RA      Robertson J.A., Bhattacharyya S., Ing N.H.;
RT      "Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and
RT      glyceraldehyde 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";
RL      J. Steroid Biochem. Mol. Biol. 67:285-292(1998).

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| |
|--|
| RESULT 2 |
| Q6LD50 |
| ID Q6LD50 PRELIMINARY; PRT; 79 AA. |
| AC Q6LD50; |
| DT 05-JUL-2004 (TREMBLrel. 27, Created) |
| DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update) |
| DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update) |
| DE Apolipoprotein A1 homolog protein (Fragment). |
| GN Name=apolipoprotein A1 homolog; |
| OS Mus sp. |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae |

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OX  NCBI_TaxID=10095;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96062440; PubMed=7488287;
RA  Merrill J.T., Rivkin E., Shen C., Lahita R.G.;
RT  "Selection of a gene for apolipoprotein A1 using autoantibodies from a
RT  patient with systemic lupus erythematosus.";
RL  Arthritis Rheum. 38:1655-1659(1995).
DR  EMBL; S80442; AAB35539.1; -.
DR  InterPro; IPR009074; Apolipo_A_E_C3.
KW  Lipoprotein.
FT  NON TER      79
SQ  SEQUENCE      79 AA;  9583 MW;  33CA72DA854A150A CRC64;

      Query Match      35.8%;  Score 226;  DB 2;  Length 79;
      Best Local Similarity  80.0%;  Pred. No. 1e-10;
      Matches  40;  Conservative  8;  Mismatches  2;  Indels  0;  Gaps  0;

Qy  70 EFDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKV 119
    :|||||: :|||:||||| :|||:||||| :|||:||||| :|||:|||||
Db  1 DFDNLEKETDWRQEMNKDLEEVKQVQPYLDEFQKKKEDVELYRQKV 50

RESULT 3
AAB35539
ID  AAB35539  PRELIMINARY;      PRT;      79 AA.
AC  AAB35539;
DT  02-MAR-2004 (TrEMBLrel. 27, Created)
DT  02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT  02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE  Apolipoprotein A1 homolog (Fragment).
OS  Mus sp.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10095;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96062440; PubMed=7488287;
RA  Merrill J.T., Rivkin E., Shen C., Lahita R.G.;
RT  "Selection of a gene for apolipoprotein A1 using autoantibodies from a
RT  patient with systemic lupus erythematosus.";
RL  Arthritis Rheum. 38:1655-1659(1995).
DR  EMBL; S80442; AAB35539.1; -.
FT  NON TER      1
SQ  SEQUENCE      79 AA;  9583 MW;  33CA72DA854A150A CRC64;

      Query Match      35.8%;  Score 226;  DB 2;  Length 79;
      Best Local Similarity  80.0%;  Pred. No. 1e-10;
      Matches  40;  Conservative  8;  Mismatches  2;  Indels  0;  Gaps  0;

Qy  70 EFDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKV 119
    :|||||: :|||:||||| :|||:||||| :|||:||||| :|||:|||||
Db  1 DFDNLEKETDWRQEMNKDLEEVKQVQPYLDEFQKKKEDVELYRQKV 50

RESULT 4
Q29248
ID  Q29248  PRELIMINARY;      PRT;      82 AA.
AC  Q29248;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Apolipoprotein A-I (Fragment).
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Small intestine;
RX  MEDLINE=96327607; PubMed=8672129;
RA  Winteroe A.K., Fredholm M., Davies W.;
RT  "Evaluation and characterization of a porcine small intestine cDNA
```

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RT  library.";
RL  Mamm. Genome 7:509-517(1996).
DR  EMBL; F14858; CAA23298.1; -.
DR  GO; GO:0005576; C:extracellular; IEA.
DR  GO; GO:0008289; F:lipid binding; IEA.
DR  GO; GO:0006869; P:lipid transport; IEA.
DR  GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR  InterPro; IPR000074; Apolipoprotein.
DR  InterPro; IPR009074; Apolipo_A_E_C3.
DR  Pfam; PF01442; Apolipoprotein; 1.
KW  Lipoprotein.
FT  NON TER      82
SQ  SEQUENCE      82 AA;  9168 MW;  24625C65CBFFEDD8 CRC64;

      Query Match      34.4%;  Score 217;  DB 2;  Length 82;
      Best Local Similarity  70.7%;  Pred. No. 5.5e-10;
      Matches  41;  Conservative  5;  Mismatches  12;  Indels  0;  Gaps  0;

Qy  2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSK 59
    :|||||: :|||:||||| :|||:||||| :|||:||||| :|||:|||||
Db  25 DDFXSPWDRVKDFXTVYVDAIKDSGRDYXAOFEASALGKHLNLKLLXNXDSLGTFTK 82

RESULT 5
Q9UCT8
ID  Q9UCT8  PRELIMINARY;      PRT;      26 AA.
AC  Q9UCT8;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Sperm activating protein subunit I, apolipoprotein A1, SPAP subunit I
DE  (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=91369902; PubMed=1909888;
RA  Akerlof E., Jornvall H., Slotte H., Pousette A.;
RT  "Identification of apolipoprotein A1 and immunoglobulin as components
RT  of a serum complex that mediates activation of human sperm motility.";
RL  Biochemistry 30:8986-8990(1991).
DR  GO; GO:0005576; C:extracellular; IEA.
DR  GO; GO:0008289; F:lipid binding; IEA.
DR  GO; GO:0006869; P:lipid transport; IEA.
DR  GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR  InterPro; IPR000074; Apolipoprotein.
DR  InterPro; IPR009074; Apolipo_A_E_C3.
DR  Pfam; PF01442; Apolipoprotein; 1.
FT  NON TER      1
FT  NON TER      26
SQ  SEQUENCE      26 AA;  2930 MW;  64921A333E768D27 CRC64;

      Query Match      22.3%;  Score 141;  DB 2;  Length 26;
      Best Local Similarity  100.0%;  Pred. No. 0.00017;
      Matches  26;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1 DEFPQSPWDRVKDLATVYVDVLKDSG 26
    |||||
Db  1 DEFPQSPWDRVKDLATVYVDVLKDSG 26

RESULT 6
Q9PRR6
ID  Q9PRR6  PRELIMINARY;      PRT;      34 AA.
AC  Q9PRR6;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Apolipoprotein A1 (Fragment).
OS  Anser anser (domestic goose).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



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DR EMBL; U52030; AAC50441.1; -.
DR HSSP; P02649; INFN.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein_1.
DR KW Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
KW Plasma; Repeat; VLDL.
FT NON TER 1 1
FT DOMAIN 89 99 LDL receptor binding (Potential).
FT DOMAIN 93 96 Heparin-binding (By similarity).
FT DOMAIN 11 >107 8 X 22 AA approximate tandem repeats.
FT REPEAT 11 32 1.
FT REPEAT 33 54 2.
FT REPEAT 55 76 3.
FT REPEAT 77 98 4.
FT REPEAT 99 >107 5.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 12382 MW; E1D38C32F5AACB23 CRC64;

Query Match 13.5%; Score 85; DB 1; Length 107;
Best Local Similarity 29.0%; Pred. No. 24;
Matches 18; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

Qy 58 SKLREQLGPVVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMLYRQ 117
Db 25 SELEEQLSPVAEETRARLSKELQAAQARLGADMEDVRSRLVQYRSEVQAMLGQSTEEELRA 84

Qy 118 KV 119
Db 85 RL 86

RESULT 10
APE_SAI SC STANDARD; PRT; 107 AA.
AC Q28995;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein E (Apo-E) (Fragment).
GN Name=APOE;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96225955; PubMed=86355577;
RA Morelli L., Wei L., Amorim A., McDermid J., Abee C.R., Frangione B.,
RA Walker L.C., Levy E.;
RT "Cerebrovascular amyloidosis in squirrel monkeys and rhesus monkeys:
RT apolipoprotein E genotype.";
RL FEBS Lett. 379:132-134(1996).
CC -!- FUNCTION: Mediates the binding, internalization, and catabolism of
CC lipoprotein particles. It can serve as a ligand for the LDL (apo
CC B/E) receptor and for the specific apo-E receptor (chylomicron
CC remnant) of hepatic tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Secreted in plasma.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U52029; AAC50442.1; -.
DR HSSP; P02649; INFN.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
```

```
DR Pfam; PF01442; Apolipoprotein; 1.
KW Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
KW Plasma; Repeat; VLDL.
FT NON TER 1 1
FT DOMAIN 89 99 LDL receptor binding (Potential).
FT DOMAIN 93 96 Heparin-binding (By similarity).
FT DOMAIN 11 >107 8 X 22 AA approximate tandem repeats.
FT REPEAT 11 32 1.
FT REPEAT 33 54 2.
FT REPEAT 55 76 3.
FT REPEAT 77 98 4.
FT REPEAT 99 >107 5.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 12328 MW; FF88CED47BD18F7C CRC64;

Query Match 13.2%; Score 83; DB 1; Length 107;
Best Local Similarity 33.3%; Pred. No. 35;
Matches 16; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

Qy 58 SKLREQLGPVVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQ 105
Db 25 SELEEQLSPVAEETRARLSKELQAAQARLGADMEDVRSRLAQYRSEVQ 72

RESULT 11
O07516
ID O07516 PRELIMINARY; PRT; 118 AA.
AC O07516; Q796U9;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein yhaH.
GN Name=yhaH; OrderedLocusNames=BSU10000;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mael C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
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ID O68959 PRELIMINARY; PRT; 118 AA.
AC O68959;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ST448;
RA Beall B.W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF058802; AAC14134.1; -.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13597 MW; 744443E4DD757559 CRC64;

Query Match 12.0%; Score 76; DB 2; Length 118;
Best Local Similarity 29.0%; Pred. No. 1.4e+02;
Matches 31; Conservative 24; Mismatches 36; Indels 16; Gaps 5;

QY 17 VYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLE 76
Db | | | | : : | | | : : : | | : : | | : : | |
5 VAVAVL---GAGFANQTEVKAAEKKEVA-----DSNASSVAKLYNQIADLTDKNGEYLE 56
QY 77 KETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEM---ELYRQKVE 120
Db : | : | | : : : : | | : : : : : : : : : :
57 RIEE--LEERQKNLEKLERQSQVAAD---KHYQEQVKKHQYKQE 98
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 13:20:25 ; Search time 157 Seconds
(without alignments)
274.188 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_144
Perfect score: 631
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LDDFQKKWQEMELYRQKVE 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1197155

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | % | | Query | | Description | |
|------------|-------|-------|--------|----|----------|-------|--|-------------|-----------|
| Result No. | Score | Match | Length | DB | ID | | | | |
| 1 | 476.5 | 75.5 | 120 | 4 | AAU30469 | | | Aau30469 | Novel hum |
| 2 | 476.5 | 75.5 | 120 | 4 | AAU30267 | | | Aau30267 | Novel hum |
| 3 | 410 | 65.0 | 119 | 4 | AAU30468 | | | Aau30468 | Novel hum |
| 4 | 197 | 31.2 | 65 | 6 | ABP76131 | | | Abp76131 | Human GEN |
| 5 | 193 | 30.6 | 42 | 2 | AAR20164 | | | Aap20164 | Apo AI po |
| 6 | 162 | 25.7 | 64 | 5 | ABP31744 | | | Abp31744 | Human apo |
| 7 | 138 | 21.9 | 32 | 2 | AAR20165 | | | Aar20165 | Apo AI po |
| 8 | 137 | 21.7 | 26 | 7 | ADE76474 | | | Ade76474 | ApoAI G* |
| 9 | 123 | 19.5 | 85 | 8 | ADP87441 | | | Adp87441 | Monkey ap |
| 10 | 119 | 18.9 | 85 | 8 | ADP87442 | | | Adp87442 | Human apo |
| 11 | 119 | 18.9 | 85 | 8 | ADP87440 | | | Adp87440 | Baboon ap |
| 12 | 118 | 18.7 | 22 | 1 | AAP92072 | | | Aap92072 | Apolipopr |
| 13 | 116 | 18.4 | 21 | 1 | AAP90956 | | | Aap90956 | Apo AI ep |
| 14 | 108 | 17.1 | 84 | 2 | AAY42554 | | | Aay42554 | Apolipopr |
| 15 | 107 | 17.0 | 85 | 8 | ADP87439 | | | Adp87439 | Pig apoli |
| 16 | 104 | 16.5 | 26 | 4 | AAG62609 | | | Aag62609 | Apolipopr |
| 17 | 101.5 | 16.1 | 107 | 8 | ADP87432 | | | Adp87432 | Rat apoli |
| 18 | 101.5 | 16.1 | 107 | 8 | ADP87431 | | | Adp87431 | Rat apoli |
| 19 | 101 | 16.0 | 85 | 8 | ADP87438 | | | Adp87438 | Chicken a |
| 20 | 97 | 15.4 | 19 | 1 | AAP92073 | | | Aap92073 | Apolipopr |
| 21 | 96.5 | 15.3 | 95 | 6 | ABP70773 | | | Abp70773 | Human apo |
| 22 | 94 | 14.9 | 30 | 7 | ADC29665 | | | Adc29665 | Antioxida |
| 23 | 94 | 14.9 | 30 | 7 | ADC29666 | | | Adc29666 | Antioxida |
| 24 | 92 | 14.6 | 18 | 7 | ADC29658 | | | Adc29658 | Antioxida |
| 25 | 91 | 14.4 | 16 | 2 | AAR72706 | | | Aar72706 | Human apo |

| | | | | | | | |
|----|----|------|-----|---|----------|----------|-----------|
| 26 | 91 | 14.4 | 16 | 2 | AAR34033 | Aar34033 | Sequence |
| 27 | 91 | 14.4 | 16 | 2 | AAU27065 | Aay27065 | Peptide S |
| 28 | 89 | 14.1 | 16 | 6 | ABP57175 | Abp57175 | Breast ca |
| 29 | 89 | 14.1 | 30 | 7 | ADC29668 | Adc29668 | Antioxida |
| 30 | 89 | 14.1 | 30 | 7 | ADC29664 | Adc29664 | Antioxida |
| 31 | 87 | 13.8 | 17 | 8 | ADH35704 | Adh35704 | Apolipopr |
| 32 | 87 | 13.8 | 17 | 8 | ADH35715 | Adh35715 | Apolipopr |
| 33 | 87 | 13.8 | 18 | 7 | ADC29657 | Adc29657 | Antioxida |
| 34 | 87 | 13.8 | 18 | 7 | ADC29660 | Adc29660 | Antioxida |
| 35 | 86 | 13.6 | 30 | 7 | ADC29667 | Adc29667 | Antioxida |
| 36 | 86 | 13.6 | 30 | 7 | ADC29671 | Adc29671 | Antioxida |
| 37 | 85 | 13.5 | 30 | 7 | ADC29669 | Adc29669 | Antioxida |
| 38 | 85 | 13.5 | 30 | 7 | ADC29670 | Adc29670 | Antioxida |
| 39 | 84 | 13.3 | 18 | 7 | ADC29663 | Adc29663 | Antioxida |
| 40 | 84 | 13.3 | 18 | 7 | ADC29659 | Adc29659 | Antioxida |
| 41 | 84 | 13.3 | 96 | 8 | ADP87419 | Adp87419 | Tupala gl |
| 42 | 84 | 13.3 | 107 | 8 | ADP87437 | Adp87437 | Mouse apo |
| 43 | 84 | 13.3 | 107 | 8 | ADP87433 | Adp87433 | Mouse apo |
| 44 | 84 | 13.3 | 107 | 8 | ADP87436 | Adp87436 | Mouse apo |
| 45 | 84 | 13.3 | 107 | 8 | ADP87434 | Adp87434 | Mouse apo |

ALIGNMENTS

RESULT 1
AAU30469

ID AAU30469 standard; protein; 120 AA.

XX

AC AAU30469;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #960.

XX

KW Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US008656.

XX

PR 18-APR-2000; 2000US-00552929.

PR 26-JAN-2001; 2001US-00770160.

XX

(HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.

XX

PS Claim 20; Page 297; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell


```

Query Match      65.0%; Score 410; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.9e-30;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

| Qy | 43 | NLKL | LDNW | DSVT | STFS | KLRQ | LGPT | QDEF | WDNL | EKET | ETGL | QEMS | KDLE | EVKAK | VQPY | LD | 102 |
|----|----|------|--|--|--|--|--|--|--|--|--|--|--|--|------------------------------|----|-----|
| Qy | | | | | | | | | | | | | | | | | |
| Db | 2 | NLKL | LDNW <td>DSVT <td>STFS <td>KLRQ <td>LGPT <td>QDEF <td>WDNL <td>EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td></td></td></td></td></td></td></td> | DSVT <td>STFS <td>KLRQ <td>LGPT <td>QDEF <td>WDNL <td>EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td></td></td></td></td></td></td> | STFS <td>KLRQ <td>LGPT <td>QDEF <td>WDNL <td>EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td></td></td></td></td></td> | KLRQ <td>LGPT <td>QDEF <td>WDNL <td>EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td></td></td></td></td> | LGPT <td>QDEF <td>WDNL <td>EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td></td></td></td> | QDEF <td>WDNL <td>EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td></td></td> | WDNL <td>EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td></td> | EKET <td>ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td></td> | ETGL <td>QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td></td> | QEMS <td>KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td></td> | KDLE <td>EVKAK <td>VQPY <td>LD</td> <td>61</td> </td></td> | EVKAK <td>VQPY <td>LD</td> <td>61</td> </td> | VQPY <td>LD</td> <td>61</td> | LD | 61 |

QY 103 DFQKKWQEEMLYRQKVE 120
|||
Db 62 DFQKKWQEEMLYRQKVE 79

RESULT 4
ABP76131
ID ABP76131 standard; protein; 65 AA.

DT 21-FEB-2003 (first entry)

DE Human GENSET protein SEQ ID 457.

Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiac; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal.

OS Homo sapiens.

PN WO200283898-A1.

PD 24-OCT-2002.

PF 18-APR-2001; 2001WO-IB000914.

PR 18-APR-2001; 2001WO-IB000914.

PA (GEST) GENSET.

PI Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;
XX
DR WPI; 2003-075548/07.

New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the PT toxicity.

PS Claim 14; Page 535; 735pp; English.

The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity

SQ Sequence 65 AA;

```
Query Match          31.2%; Score 197; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

| Qy | 1 | DEPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA | 37 |
|----------------|----|--------------------------------------|----|
| | | | |
| D _b | 25 | DEPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA | 61 |

RESULT 5
AAR20164

| | | |
|----|---------------------------------|---------------------------|
| ID | AAR20164 | standard; peptide; 42 AA. |
| XX | | |
| AC | AAR20164; | |
| XX | | |
| DT | 25-MAR-2003 | (revised) |
| DT | 01-APR-1992 | (first entry) |
| XX | | |
| DE | Apo AI polypeptide (A). | |
| XX | | |
| KW | Monoclonal antibody; MAB AI-11; | epitope; diagnosis. |
| XX | | |
| OS | Synthetic. | |

| | Key | Location/Qualifiers |
|----|---------|---------------------|
| FH | | |
| FT | Peptide | 1. .28 |
| FT | Peptide | 2. .28 |
| FT | Peptide | 7. .28 |
| FT | Peptide | 10. .28 |
| FT | Peptide | 11. .42 |
| FT | Peptide | 11. .28 |
| FT | Peptide | 13. .28 |

PN WO9118619-A.

PD 12-DEC-1991.

PF 07-JUN-1990; 90US-00534761.

07-JUN-1990; 90US-00534761.
(SCRI) SCRIPPS CLINIC & RES.
Curtiss LK, Banka CL, Bonnet DJ, Smith RS;
WPI; 1992-007201/01.
New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo
in vascular fluid samples and increase LCAT-mediated cholesterol
esterification in humans.
Claim 2; Page 68; 87pp; English.
The peptides represented in AAR20164-65 are capable of immunologically
mimicking an Apo AI epitope. They are useful in diagnosis and detection
of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is
useful in therapeutic methods for increasing LCAT- mediated cholesterol
esterification in humans. The Apo AI polypeptide is selected from the
peptides indicated in the features and includes amino acids 13-28
defining a conserved native epitope on Apo AI capable of immunoreacting
with monoclonal antibody MAB AI-11. (Updated on 25-MAR-2003 to correct
field.)

| | | | | |
|-----------------------|--------------|--------------------|---------------|------------|
| Query Match | 30.6% | Score 193; | DB 2; | Length 42; |
| Best Local Similarity | 100.0%; | Pred. No. 1.3e-10; | | |
| Matches 37; | Conservative | 0; | Mismatches 0; | Indels 0; |
| | | | Gaps | 0; |

84 QY QEMSKDLEEVKAKVQPYLDDFQKKQOEEMELYRQKVE 120
1 Db QEMSKDLEEVKAKVQPYLDDFQKKQOEEMELYRQKVE 37

RESULT 6
ABP31744
ID ABP31744 standard; protein; 64 AA.

DT 08-JUL-2002 (first entry)

Human apolipoprotein-like ORF717 protein, SEQ ID NO:1434.

KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide.
XX
OS Homo sapiens.
XX
PN WO200190366-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US017076.
XX
PR 24-MAY-2000; 2000US-0206690P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Leach MD, Shimkets RA;
XX
DR WPI; 2002-106200/14.
DR N-PSDB; ABN75770.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation.
XX
PS Claim 10; Page 625; 2508pp; English.
XX
CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN79587 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases
XX

SQ Sequence 64 AA;
Query Match 25.7%; Score 162; DB 5; Length 64;
Best Local Similarity 75.0%; Pred. No. 1.6e-07;
Matches 30; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Oy 2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ 41
: ||| ||||| ||||| :||||:||||:||||| |||:
Db 25 DEPQSQMDRVKDFATVYVDVAVKDSGRNYVSQFESSTLGQQ 64
RESULT 7
AAR20165
ID AAR20165 standard; protein; 32 AA.
XX
AC AAR20165;
XX
DT 25-MAR-2003 (revised)
DT 01-APR-1992 (first entry)
XX
DE Apo AI polypeptide (B).
XX
KW Monoclonal antibody; MAB AI-14; epitope; diagnosis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .32
FT Peptide 1. .21
FT Peptide 5. .28
FT Peptide 5. .21
FT Peptide 6. .28
FT Peptide 6. .21
FT Misc-difference 11
FT /label= GLU, PHE
XX
PN WO9118619-A.
XX
PD 12-DEC-1991.
XX
PF 07-JUN-1990; 90US-00534761.
XX
PR 07-JUN-1990; 90US-00534761.
XX
PA (SCRI) SCRIPPS CLINIC & RES.
PI Curtiss LK, Banka CL, Bonnet DJ, Smith RS;
XX
DR WPI; 1992-007201/01.
XX
PT New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo AI
PT in vascular fluid samples and increase LCAT-mediated cholesterol
PT esterification in humans.
XX
PS Claim 5; Page 68; 87pp; English.
XX
CC The peptides represented in AAR20164-65 are capable of immunologically
CC mimicking an Apo AI epitope. They are useful in diagnosis and detection
CC of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is
CC useful in therapeutic methods for increasing LCAT- mediated cholesterol
CC esterification in humans. The Apo AI polypeptide is selected from the
CC peptides indicated in the features and includes amino acids 6-21 defining
CC a conserved native epitope on Apo AI capable of immunoreacting with
CC monoclonal antibody MAB AI-4. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 32 AA;
Query Match 21.9%; Score 138; DB 2; Length 32;
Best Local Similarity 96.3%; Pred. No. 1.2e-05;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 94 KAKVQPYLDDDFQKKWQEEEMELYRQKVE 120

Db 1 KAKVQPYLDDXQKKWQEEEMELYRQKVE 27
RESULT 8
ADE76474
ID ADE76474 standard; peptide; 26 AA.
XX
AC ADE76474;
XX
DT 29-JAN-2004 (first entry)
XX
DE ApoAI G* amphipathic helical domain-derived peptide - SEQ ID 21.
XX
KW G-type; atherosclerosis; inflammatory; G* amphipathic helix;
KW antiarteriosclerotic; antirheumatic; antiarthritic; immunosuppressive;
KW dermatological; antiinflammatory; osteopathic; neuroprotective;
KW nootropic; anti-HIV; virucide; antibacterial; rheumatoid arthritis;
KW systemic lupus erythematosus; polyarteritis nodosa; osteoporosis;
KW Alzheimer's disease; AIDS; infection; apoAI.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..26 /note= "Optionally D-form residue"
FT Modified-site 1 /note= "Optional N-terminal acetyl"
FT Modified-site 26 /note= "Optional C-terminal amide"
FT
XX
PN US2003191057-A1.
XX
PD 09-OCT-2003.
XX
PF 05-APR-2002; 2002US-00120508.
XX
PR 05-APR-2002; 2002US-00120508.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Fogelman AM, Navab M;
XX
DR WPI; 2003-831662/77.
XX
PT New G-type polypeptides for preventing or ameliorating symptoms of
PT atherosclerosis or pathologies associated with an inflammatory responses
PT e.g. rheumatoid arthritis, osteoporosis, Alzheimer's disease, AIDS or
PT infections.
XX
PS Claim 7; SEQ ID NO 21; 29pp; English.
XX
CC The invention relates to a novel isolated G-type polypeptide that
CC ameliorates a symptom of atherosclerosis or other pathology associated
CC with an inflammatory response comprising an amphipathic helical peptide
CC having charged residues on the polar face of the peptide and possessing a
CC wide non-polar face. The polypeptide of the invention demonstrates
CC antiarteriosclerotic, antirheumatic, antiarthritic, immunosuppressive,
CC dermatological, antiinflammatory, osteopathic, neuroprotective,
CC nootropic, anti-HIV, virucide and antibacterial activities. The
CC composition and methods of the invention may be useful in preventing or
CC ameliorating one or more symptoms of atherosclerosis and/or pathologies
CC characterised by an inflammatory response such as rheumatoid arthritis,
CC systemic lupus erythematosus, polyarteritis nodosa, osteoporosis,
CC Alzheimer's disease, AIDS or infection. The current sequence is that of
CC the apoAI G* amphipathic helical domain-derived peptide of the invention.
XX
SQ Sequence 26 AA;
Query Match 21.7%; Score 137; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.le-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WDRVKDLATVYVDVLKDSGRDYVSQF 33
Db 1 WDRVKDLATVYVDVLKDSGRDYVSQF 26
RESULT 9
ADP87441
ID ADP87441 standard; protein; 85 AA.
XX
AC ADP87441;
XX
DT 09-SEP-2004 (first entry)
XX
DE Monkey apolipoprotein A (APO-A) precursor protein.
XX
KW Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW monkey.
XX
OS Macaca fascicularis.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX
DR WPI; 2004-480967/45.
XX
PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 48; 113pp; English.
XX
CC The invention relates to a browseable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recognizer and an output.
CC The invention also provides a method of operation for use with a
CC browseable biological database system. The browseable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC monkey apolipoprotein A (APO-A) IV precursor protein. This sequence is
CC used to illustrate the method of the invention.
XX
SQ Sequence 85 AA;
Query Match 19.5%; Score 123; DB 8; Length 85;
Best Local Similarity 31.8%; Pred. No. 0.00095;
Matches 27; Conservative 23; Mismatches 35; Indels 0; Gaps 0;
QY 36 SALGKQLNLKLLDNWDSVTSTFSLREQLGPGVTQFEWDNLEKETEGLRQEMSKDLEEVKA 95
Db 1 SELTQQLNALFQDKLGEVNTYAGDLQKKLVFPFATELHERLAKDSEKLEKEIRKELEVRA 60
QY 96 KVQPYLDDFQKKWQEEEMELYRQKVE 120
Db 61 RLLPHANEVSKIGENVRELOQRLE 85
RESULT 10
ADP87442

ID ADP87442 standard; protein; 85 AA.
XX
AC ADP87442;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human apolipoprotein A (APO-A) precursor protein.
XX
KW Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX
DR WPI; 2004-480967/45.
XX
PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 49; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recognizer and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC human apolipoprotein A (APO-A) IV precursor protein. This sequence is
CC used to illustrate the method of the invention.
XX
SQ Sequence 85 AA;

Query Match 18.9%; Score 119; DB 8; Length 85;
Best Local Similarity 29.4%; Pred. No. 0.0022;
Matches 25; Conservative 25; Mismatches 35; Indels 0; Gaps 0;

QY 36 SALGKQLNLKLLDNWDSVTSTFSLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA 95
Db 1 SELTQQLNALFQDKLGEVNTYAGDLQKKLVFPFATELHERLAKDSEKLKEIGKELEELRA 60

QY 96 KVQPYLDDFQKKWQEEEMELYRQKVE 120
Db 61 RLLPHANEVSKIGDNLRELQQRLE 85

RESULT 11
ADP87440
ID ADP87440 standard; protein; 85 AA.
XX
AC ADP87440;
XX
DT 09-SEP-2004 (first entry)
XX
DE Baboon apolipoprotein A (APO-A) IV precursor protein.

XX Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW baboon.
XX
OS Papio anubis.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX
DR WPI; 2004-480967/45.
XX
PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 47; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recognizer and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC baboon apolipoprotein A (APO-A) IV precursor protein. This sequence is
CC used to illustrate the method of the invention.
XX
SQ Sequence 85 AA;

Query Match 18.9%; Score 119; DB 8; Length 85;
Best Local Similarity 30.6%; Pred. No. 0.0022;
Matches 26; Conservative 24; Mismatches 35; Indels 0; Gaps 0;

QY 36 SALGKQLNLKLLDNWDSVTSTFSLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA 95
Db 1 SELTQQLNALFQDKLGEVNTYAGDLQKKLVFPFATELHERLAKDSEKLKEIRKELEVRA 60

QY 96 KVQPYLDDFQKKWQEEEMELYRQKVE 120
Db 61 RLLPHANEVSKIGENVRELQQRLE 85

RESULT 12
AAP92072
ID AAP92072 standard; peptide; 22 AA.
XX
AC AAP92072;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 10-APR-1990 (first entry)
XX
DE Apolipoprotein AI (Apo AI) polypeptide.
XX
KW Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL;
KW coronary artery disease; CAD; Apo AI epitope.
XX
OS Homo sapiens.


```
XX FH Key Location/Qualifiers
FT Peptide 1..22 /label= AI90-111
FT Peptide /label= AI90-111
FT Peptide 1..22 /label= AI90-111
FT Peptide 1..16 /label= AI90-105
FT Peptide 4..12 /label= AI93-101
FT Peptide 6..16 /label= AI95-105
FT Peptide 7..12 /label= AI96-101
FT Peptide 11..16 /label= AI100-105
FT Peptide 12..22 /label= AI101-111
XX
PN WO8904486-A.
XX
XX PD 18-MAY-1989.
XX
XX PF 02-NOV-1988; 88WO-US003903.
XX
XX PR 03-NOV-1987; 87US-00116248.
XX
XX PA (SCRI ) SCRIPPS CLINIC & RES FOUND.
XX
XX PI Curtiss LK, Smith RR;
XX WPI; 1989-165740/22.
DR
XX
PT New monoclonal antibody and polypeptide antigens - directed against APO
PT AI-HDL epitope, useful in diagnostic assays.
XX
XX PS Claim 2; Table 1-2; 62pp; English.
XX
XX CC AI90-111 and smaller peptides contained within this sequence. AI95-105,
CC AI190-105 and AI190-111 are specifically claimed. Such Apo AI peptides
CC are capable of immunologically mimicking a native conserved Apo AI
CC epitope. They may be helpful in the diagnosis of risk of coronary heart
CC disease. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25
CC -MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX SQ Sequence 22 AA;
Query Match 18.7%; Score 118; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 LEEVKAKVQPYLDDFQKKWQEE 111
Db 1 LEEVKAKVQPYLDDFQKKWQEE 22
RESULT 13
AAP90956
ID AAP90956 standard; peptide; 21 AA.
XX
XX AC AAP90956;
XX
XX DT 25-MAR-2003 (revised)
XX DT 19-FEB-1990 (first entry)
XX
XX DE Apo AI epitope.
XX
XX KW High density lipoproteins.
XX
XX OS Synthetic.
XX
XX PN WO8909403-A.
```

```
XX PD 05-OCT-1989.
XX
XX PF 27-MAR-1989; 89WO-US001262.
XX
XX PR 29-MAR-1988; 88US-00174698.
XX
XX PA (SCRI ) SCRIPPS CLINIC & RES FOUND.
XX
XX PI Curtiss LK, Smith RS;
XX WPI; 1989-309644/42.
DR
XX
PT Apo lipoprotein peptide and monoclonal antibody against it - used to
PT assay peptide in vascular fluid to identify risk of coronary artery
PT disease.
XX
XX PS Claim 2; Page 41; 49pp; English.
XX
XX CC Apo AI contains the sequence below (Claim 1 claims AAs 1-15). There is an
CC inverse correlation between plasma levels of Apo AI and coronary artery
CC disease risk. The monoclonal antibody recognises this epitope on native
CC Apo AI. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 21 AA;
Query Match 18.4%; Score 116; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEPPQSPWDRVKDLATVYVDV 21
Db 1 DEPPQSPWDRVKDLATVYVDV 21
RESULT 14
AAY42554
ID AAY42554 standard; peptide; 84 AA.
XX
XX AC AAY42554;
XX
XX DT 20-DEC-1999 (first entry)
XX
XX DE Apolipoprotein A-IV derived lipid oxidation suppressant peptide #2.
XX
XX KW Cholesterol; cardiovascular disease; heart disease; atherosclerosis;
KW lipoprotein; angina; myocardial infarction; stroke; thrombosis;
KW antioxidant; hypolipidaemic; apolipoprotein.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 84
XX FT /note= "Optionally has a C-terminal amide"
XX
XX PN WO9950286-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 25-MAR-1999; 99WO-US006580.
XX
XX PR 31-MAR-1998; 98US-0080131P.
XX
XX PA (UYCI-) UNIV CINCINNATI.
XX
XX PI Hui DY, Tso P;
XX
XX WPI; 1999-580739/49.
DR
XX
PT Treating conditions associated with lipid oxidation or preventing
PT oxidation in lipid-containing food, lipid containing pharmaceuticals or
PT cosmetic or dermatological compositions.
```

Claim 4; Page 53; 73pp; English.

This sequence represents a peptide (#2) derived from apolipoprotein (apo) A-IV with lipid oxidation inhibitory activity. Lipid oxidation plays a role in the development of atherosclerosis, a main cause of coronary heart disease. Atherosclerosis is thought to begin with local injury to the arterial endothelium, followed by proliferation of arterial smooth muscle cells, along with deposition of lipid and accumulation of foam cells in the lesion. As the atherosclerotic plaque develops, it progressively occludes more and more blood vessel and can eventually lead to ischaemia or infarction. Both the plasma concentration and qualitative characteristics of low density lipoproteins (LDL) are risk factors in atherogenesis. Oxidation causes important changes in the primary structure of the main LDL apolipoprotein, apolipoprotein B100 (apo B-100). These changes, by helping LDL absorption by macrophages, causes the intracellular accumulation of esters of cholesterol and the formation of foam cells, with subsequent development of the atherosclerotic plaque. The apo A-IV derived peptides can be used for inhibiting lipid oxidation. The peptides can be used for treating conditions associated with lipid oxidation. For example, they can be used for treating or inhibiting the progression of atherosclerosis. They can also be used for preventing oxidation in lipid-containing foods, lipid-containing pharmaceuticals or cosmetic or dermatological compositions. As these peptides comprise specific portions of the native apo A-IV protein, there should be no immunogenicity problems with their administration to humans.

```

XX Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 46; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recogniser and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is pig
CC apolipoprotein A (APO-A) IV precursor protein. This sequence is used to
CC illustrate the method of the invention.
XX
SQ Sequence 85 AA;

      Query Match          17.0%; Score 107; DB 8; Length 85;
      Best Local Similarity 27.4%; Pred. No. 0.029;
      Matches 23; Conservative 25; Mismatches 36; Indels 0; Gaps 0;

QY    36 SALGKQLNLKLLDNWDSVTSTFSKLREQLGPVQTQEFWDNLEKETETGLRQEMSKDLSEVKA 95
      |||::||| | : |::|| | : |::|| | : |::|| | : |::|||::|
Db    1 SELTQQNLTLFQDKLGEVNTYTEDLQKKLVFPATELHERLTOKDSEKLKEEIRRELSELRA 60

QY    96 KVQPYLDDFQKKWQEEMELYRKQV 119
      ::|::: : :| : : :|:::
Db    61 RLLPHATEVSOKIGDENVRELQORL 84

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OM protein - protein search, using sw model

Run on: December 21, 2004, 12:34:05 ; Search time 142 Seconds
(without alignments)
302.396 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_144
Perfect score: 631
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LDDFQKQWQEMELYRQKVE 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 783582

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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| 2: | /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.* | | | | |
| 3: | /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.* | | | | |
| 4: | /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.* | | | | |
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| 8: | /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.* | | | | |
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| 19: | /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.* | | | | |
| 20: | /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.* | | | | |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length DB | ID | Description |
|------------|-------|---------------|-----------|----|---------------------------------------|
| 1 | 387.5 | 61.4 | 93 | 15 | US-10-038-854-403 Sequence 403, App |
| 2 | 387.5 | 61.4 | 93 | 15 | US-10-038-854-405 Sequence 405, App |
| 3 | 318 | 50.4 | 86 | 15 | US-10-424-599-276814 Sequence 276814, |
| 4 | 227 | 36.0 | 43 | 15 | US-10-465-789A-89 Sequence 89, Appl |
| 5 | 162 | 25.7 | 64 | 11 | US-09-864-408A-1434 Sequence 1434, Ap |
| 6 | 137 | 21.7 | 26 | 14 | US-10-120-508-21 Sequence 21, Appl |
| 7 | 122 | 19.3 | 22 | 15 | US-10-465-789A-52 Sequence 52, Appl |
| 8 | 118 | 18.7 | 22 | 15 | US-10-465-789A-50 Sequence 50, Appl |
| 9 | 112 | 17.7 | 22 | 15 | US-10-465-789A-49 Sequence 49, Appl |
| 10 | 96.5 | 15.3 | 95 | 17 | US-10-487-096-2 Sequence 2, Appli |
| 11 | 94 | 14.9 | 30 | 14 | US-10-142-238A-40 Sequence 40, Appl |
| 12 | 94 | 14.9 | 30 | 14 | US-10-142-238A-41 Sequence 41, Appl |
| 13 | 92 | 14.6 | 18 | 14 | US-10-142-238A-33 Sequence 33, Appl |

| | | | | | | |
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| 14 | 89 | 14.1 | 16 | 17 | US-10-700-340-37 | Sequence 37, Appl |
| 15 | 89 | 14.1 | 30 | 14 | US-10-142-238A-39 | Sequence 39, Appl |
| 16 | 89 | 14.1 | 30 | 14 | US-10-142-238A-43 | Sequence 43, Appl |
| 17 | 87 | 13.8 | 17 | 15 | US-10-601-100-44 | Sequence 44, Appl |
| 18 | 87 | 13.8 | 18 | 14 | US-10-142-238A-32 | Sequence 32, Appl |
| 19 | 87 | 13.8 | 18 | 14 | US-10-142-238A-35 | Sequence 35, Appl |
| 20 | 86 | 13.6 | 30 | 14 | US-10-142-238A-42 | Sequence 42, Appl |
| 21 | 86 | 13.6 | 30 | 14 | US-10-142-238A-46 | Sequence 46, Appl |
| 22 | 85 | 13.5 | 30 | 14 | US-10-142-238A-44 | Sequence 44, Appl |
| 23 | 85 | 13.5 | 30 | 14 | US-10-142-238A-45 | Sequence 45, Appl |
| 24 | 84 | 13.3 | 18 | 14 | US-10-142-238A-34 | Sequence 34, Appl |
| 25 | 84 | 13.3 | 18 | 14 | US-10-142-238A-38 | Sequence 38, Appl |
| 26 | 83 | 13.2 | 18 | 14 | US-10-142-238A-36 | Sequence 36, Appl |
| 27 | 83 | 13.2 | 18 | 14 | US-10-142-238A-37 | Sequence 37, Appl |
| 28 | 77 | 12.2 | 90 | 15 | US-10-038-854-224 | Sequence 224, App |
| 29 | 77 | 12.2 | 90 | 15 | US-10-038-854-231 | Sequence 231, App |
| 30 | 76 | 12.0 | 107 | 14 | US-10-023-066A-92 | Sequence 92, Appl |
| 31 | 74 | 11.7 | 14 | 15 | US-10-601-100-43 | Sequence 43, Appl |
| 32 | 74 | 11.7 | 113 | 17 | US-10-480-848A-5 | Sequence 5, Appli |
| 33 | 72 | 11.4 | 62 | 9 | US-09-864-761-40424 | Sequence 40424, A |
| 34 | 68.5 | 10.9 | 92 | 16 | US-10-767-701-61738 | Sequence 61738, A |
| 35 | 67.5 | 10.7 | 72 | 16 | US-10-767-701-37365 | Sequence 37365, A |
| 36 | 67 | 10.6 | 21 | 14 | US-10-076-047A-34 | Sequence 34, Appl |
| 37 | 66.5 | 10.5 | 105 | 17 | US-10-639-067-135 | Sequence 135, App |
| 38 | 66 | 10.5 | 13 | 14 | US-10-014-340-123 | Sequence 123, App |
| 39 | 66 | 10.5 | 13 | 15 | US-10-264-309-76 | Sequence 76, Appl |
| 40 | 66 | 10.5 | 13 | 15 | US-10-601-100-36 | Sequence 36, Appl |
| 41 | 66 | 10.5 | 105 | 9 | US-09-767-215-10 | Sequence 10, Appl |
| 42 | 66 | 10.5 | 119 | 16 | US-10-767-701-58043 | Sequence 58043, A |
| 43 | 65.5 | 10.4 | 99 | 15 | US-10-674-755-16 | Sequence 16, Appl |
| 44 | 65.5 | 10.4 | 118 | 14 | US-10-136-728-32 | Sequence 32, Appl |
| 45 | 65 | 10.3 | 76 | 14 | US-10-106-698-6884 | Sequence 6884, Ap |

ALIGNMENTS

RESULT 1

US-10-038-854-403

; Sequence 403, Application US/10038854

; Publication No. US20040022781A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Li, Li

; APPLICANT: Wolenc, Adam R

; APPLICANT: Vernet, Corine

; APPLICANT: Eisen, Andrew J

; APPLICANT: Liu, Xiaohong

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Shimkets, Richard A

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spaderna, Steven K

; APPLICANT: Gorman, Linda

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Patturajan, Meera

; APPLICANT: Gusev, Vladimir Y

; APPLICANT: Gangolli, Esha A

; APPLICANT: Guo, Xiaojia S

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Rastelli, Luca

; APPLICANT: Casman, Stacie J

; APPLICANT: Boldog, Ferenc

; APPLICANT: Burgess, Catherine E

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Ellerman, Karen

; APPLICANT: Gunther, Erik

; APPLICANT: Smithson, Glennda

; APPLICANT: Millet, Isabelle

; APPLICANT: MacDougall, John R

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-230

; CURRENT APPLICATION NUMBER: US/10/038,854

; CURRENT FILING DATE: 2003-01-22

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; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 403
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-403

Query Match      61.4%; Score 387.5; DB 15; Length 93;
Best Local Similarity 74.8%; Pred. No. 2.1e-28;
Matches 80; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 14 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 73
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Db 34 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 80

RESULT 2
US-10-038-854-405
; Sequence 405, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Baha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
```

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; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 405
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-405

Query Match      61.4%; Score 387.5; DB 15; Length 93;
Best Local Similarity 74.8%; Pred. No. 2.1e-28;
Matches 80; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 14 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 73
Db 1 LATVYVDVLK-----DSVTSTFSKLREQLGPVTQEFWD 33

QY 74 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120
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RESULT 3
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; Sequence 276814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276814
; LENGTH: 86
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91983C.1.pep
US-10-424-599-276814

Query Match      50.4%; Score 318; DB 15; Length 86;
Best Local Similarity 98.4%; Pred. No. 5.5e-22;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 30
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-41

Query Match      14.9%; Score 94; DB 14; Length 30;
Best Local Similarity 95.0%; Pred. No. 0.096;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 42 LNLKLLDNWDSVTSTFSKLR 61
Db 11 LPLKLLDNWDSVTSTFSKLR 30

RESULT 13
US-10-142-238A-33
; Sequence 33, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-33

Query Match      14.6%; Score 92; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 LKLLDNWDSVTSTFSKLR 61
Db 1 LKLLDNWDSVTSTFSKLR 18

RESULT 14
US-10-700-340-37
; Sequence 37, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREAST CANCER
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
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; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-37

Query Match      14.1%; Score 89; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EQLGPVTQEFWDNLEK 77
Db 1 EQLGPVTQEFWDNLEK 16

RESULT 15
US-10-142-238A-39
; Sequence 39, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-39

Query Match      14.1%; Score 89; DB 14; Length 30;
Best Local Similarity 90.0%; Pred. No. 0.28;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 42 LNLKLLDNWDSVTSTFSKLR 61
Db 11 LPLKLLDNWDSVTSTFSKLR 30

Search completed: December 21, 2004, 12:43:40
Job time : 143 secs
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OM protein - protein search, using sw model
Run on: December 21, 2004, 13:06:21 ; Search time 38 Seconds
(without alignments)
209.425 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_144
Perfect score: 631
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LDDFQKKWQEMELYRQKVE 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 327303

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
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| 1 | 198 | 31.4 | 44 | 2 | US-08-292-870-2 Sequence 2, Appli |
| 2 | 188 | 29.8 | 64 | 2 | US-08-292-870-1 Sequence 1, Appli |
| 3 | 138 | 21.9 | 32 | 2 | US-08-292-870-3 Sequence 3, Appli |
| 4 | 124 | 19.7 | 25 | 2 | US-08-292-870-4 Sequence 4, Appli |
| 5 | 91 | 14.4 | 16 | 1 | US-07-959-946-5 Sequence 5, Appli |
| 6 | 91 | 14.4 | 16 | 1 | US-08-333-577-5 Sequence 5, Appli |
| 7 | 91 | 14.4 | 16 | 5 | PCT-US92-08634-5 Sequence 5, Appli |
| 8 | 78 | 12.4 | 110 | 1 | US-07-849-389-7 Sequence 7, Appli |
| 9 | 76 | 12.0 | 107 | 1 | US-08-182-175A-105 Sequence 105, App |
| 10 | 76 | 12.0 | 107 | 1 | US-08-474-633A-92 Sequence 92, Appl |
| 11 | 76 | 12.0 | 107 | 4 | US-08-823-771-92 Sequence 92, Appl |
| 12 | 76 | 12.0 | 107 | 5 | PCT-US92-06412-105 Sequence 105, App |
| 13 | 72 | 11.4 | 105 | 4 | US-09-513-999C-6681 Sequence 6681, Ap |
| 14 | 67.5 | 10.7 | 87 | 1 | US-08-685-764-4 Sequence 4, Appli |
| 15 | 67 | 10.6 | 13 | 5 | PCT-US94-01234-47 Sequence 47, Appl |
| 16 | 66.5 | 10.5 | 99 | 4 | US-09-543-681A-8306 Sequence 8306, Ap |
| 17 | 66.5 | 10.5 | 105 | 1 | US-08-241-853-11 Sequence 11, Appl |
| 18 | 66.5 | 10.5 | 105 | 2 | US-08-850-917-11 Sequence 11, Appl |
| 19 | 65.5 | 10.4 | 99 | 4 | US-09-147-875A-16 Sequence 16, Appl |
| 20 | 65.5 | 10.4 | 102 | 4 | US-09-513-999C-8125 Sequence 8125, Ap |
| 21 | 65 | 10.3 | 103 | 4 | US-09-134-000C-4548 Sequence 4548, Ap |
| 22 | 64.5 | 10.2 | 63 | 2 | US-08-891-837B-3 Sequence 3, Appli |
| 23 | 64.5 | 10.2 | 63 | 2 | US-08-891-837B-4 Sequence 4, Appli |
| 24 | 64 | 10.1 | 99 | 4 | US-09-270-767-44037 Sequence 44037, A |
| 25 | 63.5 | 10.1 | 50 | 3 | US-09-695-458-9 Sequence 9, Appli |
| 26 | 63 | 10.0 | 103 | 4 | US-09-270-767-57235 Sequence 57235, A |
| 27 | 63 | 10.0 | 106 | 4 | US-09-621-976-4439 Sequence 4439, Ap |

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| 28 | 62.5 | 9.9 | 101 | 2 | US-08-710-749-1 | Sequence 1, Appli |
| 29 | 62 | 9.8 | 65 | 2 | US-08-867-087B-34 | Sequence 34, Appl |
| 30 | 62 | 9.8 | 105 | 2 | US-08-743-200-2 | Sequence 2, Appli |
| 31 | 62 | 9.8 | 110 | 4 | US-09-205-258-1080 | Sequence 1080, Ap |
| 32 | 61.5 | 9.7 | 98 | 2 | US-08-479-078-7 | Sequence 7, Appli |
| 33 | 61.5 | 9.7 | 99 | 2 | US-08-710-749-10 | Sequence 10, Appl |
| 34 | 61.5 | 9.7 | 99 | 4 | US-09-147-875A-11 | Sequence 11, Appl |
| 35 | 61 | 9.7 | 66 | 2 | US-08-867-087B-70 | Sequence 70, Appl |
| 36 | 61 | 9.7 | 100 | 4 | US-09-147-875A-12 | Sequence 12, Appl |
| 37 | 60.5 | 9.6 | 37 | 3 | US-09-695-458-15 | Sequence 15, Appl |
| 38 | 60 | 9.5 | 80 | 3 | US-09-183-861-61 | Sequence 61, Appl |
| 39 | 60 | 9.5 | 80 | 3 | US-09-022-765-61 | Sequence 61, Appl |
| 40 | 60 | 9.5 | 80 | 4 | US-09-071-035-134 | Sequence 134, App |
| 41 | 60 | 9.5 | 80 | 4 | US-09-551-974A-61 | Sequence 61, Appl |
| 42 | 60 | 9.5 | 80 | 4 | US-09-565-501A-61 | Sequence 61, Appl |
| 43 | 60 | 9.5 | 80 | 4 | US-09-639-206A-61 | Sequence 61, Appl |
| 44 | 60 | 9.5 | 80 | 4 | US-09-874-923-61 | Sequence 61, Appl |
| 45 | 60 | 9.5 | 85 | 4 | US-09-134-000C-3703 | Sequence 3703, Ap |

ALIGNMENTS

RESULT 1
US-08-292-870-2
; Sequence 2, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-2
Query Match 31.4%; Score 198; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120
Db 1 RQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 38

RESULT 2
US-08-292-870-1
; Sequence 1, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-1
Query Match 29.8%; Score 188; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 EMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120
Db 1 EMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 36

RESULT 3
US-08-292-870-3
; Sequence 3, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa can be either E (Glu)
; OTHER INFORMATION: or F (Phe)"
US-08-292-870-3
Query Match 21.9%; Score 138; DB 2; Length 32;
Best Local Similarity 96.3%; Pred. No. 6.1e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 94 KAKVQPYLDDFQKKWQEEEMELYRQKVE 120
Db 1 KAKVQPYLDDXQKKWQEEEMELYRQKVE 27

RESULT 4
US-08-292-870-4
; Sequence 4, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-4

Query Match 19.7%; Score 124; DB 2; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 SKDLEEVKAKVQPYLDQFKKWQEE 111
Db 1 SKDLEEVKAKVQPYLDQFKKWQEE 25

RESULT 5
US-07-959-946-5
; Sequence 5, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.

; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-959-946-5

Query Match 14.4%; Score 91; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KVQPYLDDFQKKWQEE 111
Db 1 KVQPYLDDFQKKWQEE 16

RESULT 6
US-08-333-577-5
; Sequence 5, Application US/08333577
; Patent No. 5786206
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,577
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 234.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-333-577-5

Query Match 14.4%; Score 91; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KVQPYLDDDFQKKWQEE 111
Db 1 KVQPYLDDDFQKKWQEE 16

RESULT 7
PCT-US92-08634-5
; Sequence 5, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08634
; FILING DATE: 19921009
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-08634-5

Query Match 14.4%; Score 91; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KVQPYLDDDFQKKWQEE 111
Db 1 KVQPYLDDDFQKKWQEE 16

RESULT 8
US-07-849-389-7
; Sequence 7, Application US/07849389
; Patent No. 5525493
; GENERAL INFORMATION:
; APPLICANT: HORNES, Erik
; APPLICANT: UHLEN, Mathias
; TITLE OF INVENTION: CLONING METHOD AND KIT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/849,389
; FILING DATE: 19920519
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16787/168/DFBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-849-389-7

Query Match 12.4%; Score 78; DB 1; Length 110;
Best Local Similarity 29.0%; Pred. No. 2.1;
Matches 18; Conservative 13; Mismatches 31; Indels 0; Gaps 0;

QY 58 SKLREQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDDFQKKWQEEMLYRQ 117
Db 8 SELEEQLTPVAETRARLSKELQAAEAPLGADMEDVGRVLVQYRGEVQAMLGQSTELRV 67

QY 118 KV 119
Db 68 RL 69

RESULT 9
US-08-182-175A-105
; Sequence 105, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
```

```

; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-182-175A-105

Query Match 12.0%; Score 76; DB 1; Length 107;
Best Local Similarity 25.7%; Pred. No. 3.2;
Matches 18; Conservative 22; Mismatches 22; Indels 8; Gaps 2;

QY 59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDDFQKKWQE 110
||:|:: : || ||:|:: : :|| |::|| |::||:|
Db 7 KLKEEMAKMKDEMWMKLKEEMKKLEEKMKVMEEKMKKLEEKMKAMEDKMKWLEEKMKKKLEE 66

QY 111 EMELYRQKVE 120
:|:: :|::
Db 67 KMKVMEEEKMK 76

RESULT 10
US-08-474-633A-92
; Sequence 92, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; APPLICANT: COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; TITLE OF INVENTION: METHODS FOR INCREASING
; TITLE OF INVENTION: INCREASING THE LYSINE
; TITLE OF INVENTION: AND THREONINE CONTENT
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898

APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-182-175A-105

Query Match 12.0%; Score 76; DB 1; Length 107;
Best Local Similarity 25.7%; Pred. No. 3.2;
Matches 18; Conservative 22; Mismatches 22; Indels 8; Gaps 2;

QY 59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDDFQKKWQE 110
||:|:: : || ||:|:: : :|| |::|| |::||:|
Db 7 KLKEEMAKMKDEMWMKLKEEMKKLEEKMKVMEEKMKKLEEKMKAMEDKMKWLEEKMKKKLEE 66

QY 111 EMELYRQKVE 120
:|:: :|::
Db 67 KMKVMEEEKMK 76

RESULT 10
US-08-474-633A-92
; Sequence 92, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; APPLICANT: COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; TITLE OF INVENTION: METHODS FOR INCREASING
; TITLE OF INVENTION: INCREASING THE LYSINE
; TITLE OF INVENTION: AND THREONINE CONTENT
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-633A-92

Query Match 12.0%; Score 76; DB 1; Length 107;
Best Local Similarity 25.7%; Pred. No. 3.2;
Matches 18; Conservative 22; Mismatches 22; Indels 8; Gaps 2;

QY 59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDDFQKKWQE 110
||:|:: : || ||:|:: : :|| |::|| |::||:|
Db 7 KLKEEMAKMKDEMWMKLKEEMKKLEEKMKVMEEKMKKLEEKMKAMEDKMKWLEEKMKKKLEE 66

QY 111 EMELYRQKVE 120
:|:: :|::
Db 67 KMKVMEEEKMK 76

RESULT 11
US-08-823-771-92
; Sequence 92, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; APPLICANT: COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; METHODS FOR INCREASING
; INCREASING THE LYSINE
; AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
```

```

; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-08-823-771-92

Query Match 12.0%; Score 76; DB 4; Length 107;
Best Local Similarity 25.7%; Pred. No. 3.2;
Matches 18; Conservative 22; Mismatches 22; Indels 8; Gaps 2;

QY 59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
|||::: : ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 KLKEEMAKMKDEMWKLEEMKKLEEKMKVMEEMKKLEEKMKAMEDKMKWLEEKMKLEE 66

QY 111 EMELYRQKVE 120
:|::: :|::
Db 67 KMKVMEEMKMK 76

RESULT 13
US-09-513-999C-6681
; Sequence 6681, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6681
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6681

Query Match 11.4%; Score 72; DB 4; Length 105;
Best Local Similarity 24.2%; Pred. No. 7.7;
Matches 23; Conservative 22; Mismatches 36; Indels 14; Gaps 3;

QY 39 GKQLNLKLLD-NWDSVTSTFSKLRQLGPVTQEFWDLNLEKETEG---LRQEMSKDLEEVK 94
|||:|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 7 GKEQQLDIMNKQYQQLSERLDEILSRIAKETEEIKDLEEQLTEGQIAANEALKDLEGVI 66

QY 95 AKVQPYLDDFQ-----KKWQEEEMELYRQKV 119
:|::: :|::: :|::: :|::: :|::: :|:::
Db 67 SGLQEYLGTIKGQATQAQNECRKLRDEKETLLQRL 101

RESULT 14
US-08-685-764-4
; Sequence 4, Application US/08685764
; Patent No. 5800982
; GENERAL INFORMATION:
; APPLICANT: HASEGAWA, AKIRA
; APPLICANT: MAKI, NOBORU
; APPLICANT: YAGI, SHINTARO
; APPLICANT: KASHIWAKUMA, TOMIKO
; TITLE OF INVENTION: ANTIGENIC PEPTIDES FOR GROUPING
; TITLE OF INVENTION: HEPATITIS C VIRUS, KIT COMPRISING THE SAME AND
; TITLE OF INVENTION: METHODS FOR ITS GROUPING USING THE SAME
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,764
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/092,192
FILING DATE: 15-JUL-1993
APPLICATION NUMBER: JP 212061/92
FILING DATE: 16-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 316634/92
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 316635/92
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104754/93
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, LINDA M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 42822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-764-4

```

| | Query Match | 10.7% | Score 67.5; | DB 1; | Length 87; |
|----|--|--------|----------------|------------|------------|
| | Best Local Similarity | 24.2%; | Pred. No. 17; | | |
| | Matches 23; Conservative | 22; | Mismatches 39; | Indels 11; | Gaps 3; |
| QY | 13 DLATVVDVLKSDGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFW | : | : | : | : |
| Dd | 1 EFATGCVSII---GRLHINRAVVAPDKEVLYEAFDENEECASRAALIEE-----GORIA | : | : | : | : |

| | | |
|----|----|-------------------------------------|
| Qy | 73 | DNLEKETEGIRQEMSKOLEEVKAKVQ--PYLDDF |
| Db | 53 | EMLKSKIQGLLOQAASKOAQDTPAVOTSWPKVEQF |

```

RESULT 15
PCT-US94-01234-47
; Sequence 47, Application PC/TUS9401234
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE
; TITLE OF INVENTION: BINDING SITES
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01234
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,542
; FILING DATE: 28-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2004, 12:24:55 ; Search time 191 Seconds
(without alignments)
328.355 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_133
Perfect score: 576
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LEEYKAKVQPYLDDFQKKWQ 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 337476

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|-------------|---------------------|
| 1 | 247 | 42.9 | 56 | 2 | O02762 | O02762 ovis aries |
| 2 | 217 | 37.7 | 82 | 2 | Q29248 | Q29248 sus scrofa |
| 3 | 183 | 31.8 | 79 | 2 | Q6LD50 | Q6LD50 mus sp. apo |
| 4 | 183 | 31.8 | 79 | 2 | AAB35539 | Aab35539 mus sp. a |
| 5 | 141 | 24.5 | 26 | 2 | Q9UCT8 | Q9uct8 homo sapien |
| 6 | 106 | 18.4 | 34 | 2 | Q9PRR6 | Q9prrr6 anser anser |
| 7 | 101 | 17.5 | 20 | 1 | APAI1 ERYPA | P18647 erythrocebu |
| 8 | 101 | 17.5 | 30 | 2 | Q9QV04 | Q9qv04 rattus sp. |
| 9 | 83 | 14.4 | 107 | 1 | APE_SAISC | Q28995 saimiri sci |
| 10 | 82 | 14.2 | 107 | 1 | APE_MACMU | Q28502 macaca mula |
| 11 | 77.5 | 13.5 | 96 | 2 | Q7P280 | Q7p280 fusbacteri |
| 12 | 74.5 | 12.9 | 102 | 2 | Q9PXP4 | Q9pxp4 hepatitis c |
| 13 | 73 | 12.7 | 76 | 2 | Q6WHJ6 | Q6whj6 bacterioph |
| 14 | 73 | 12.7 | 76 | 2 | AAQ64377 | Aaq64377 bacteriop |
| 15 | 73 | 12.7 | 93 | 2 | Q81R54 | Q81r54 bacillus an |
| 16 | 73 | 12.7 | 93 | 2 | AAT31321 | Aat31321 bacillus |
| 17 | 72 | 12.5 | 102 | 2 | Q29258 | Q29258 sus scrofa |
| 18 | 68 | 11.8 | 90 | 2 | Q9LCR0 | Q9lcr0 paenibacill |
| 19 | 68 | 11.8 | 101 | 2 | Q6BMU6 | Q6bmu6 debaryomyce |
| 20 | 67 | 11.6 | 95 | 2 | P89597 | P89597 human immun |
| 21 | 66.5 | 11.5 | 79 | 2 | Q9CHE9 | Q9che9 lactococcus |
| 22 | 66 | 11.5 | 80 | 2 | Q6NK47 | Q6nk47 corynebacte |
| 23 | 66 | 11.5 | 80 | 2 | CAE48695 | Cae48695 corynebac |
| 24 | 66 | 11.5 | 104 | 2 | Q54892 | Q54892 streptococc |
| 25 | 65.5 | 11.4 | 95 | 2 | Q82VG7 | Q82vg7 nitrosomona |
| 26 | 65 | 11.3 | 102 | 2 | Q86F03 | Q86f03 schistosoma |
| 27 | 64 | 11.1 | 95 | 2 | P89581 | P89581 human immun |
| 28 | 63.5 | 11.0 | 79 | 2 | Q8FXA5 | Q8fxa5 brucella su |
| 29 | 63.5 | 11.0 | 96 | 2 | Q9TS51 | Q9ts51 sus scrofa |
| 30 | 63.5 | 11.0 | 105 | 2 | O85812 | O85812 streptococc |
| 31 | 63 | 10.9 | 69 | 1 | SEM1_ASHGO | P62499 ashbya goss |

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32      63      10.9      69      2      AAS52934      ashbya go
33      63      10.9      77      2      Q93K19      lactococcus
34      63      10.9      99      2      Q9PSS3      gallus gall
35      63      10.9      107     1      YC51_HAEIN  haemophilus
36      62.5     10.9      78      2      Q9RHF1      streptococc
37      62.5     10.9      92      2      Q73LU4      treponema d
38      62.5     10.9      92      2      AAS12283   treponema
39      62.5     10.9      96      2      Q97AV3     thermoplasm
40      62.5     10.9      98      2      Q8AWE6     oncorhynchu
41      62      10.8      92      2      Q8TYR5     methanopyru
42      62      10.8      95      2      P89588     human immun
43      62      10.8      95      2      P89596     human immun
44      62      10.8      96      2      Q7ZPL6     human immun
45      61.5     10.7      75      2      Q6U9J3     bacterioph
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ALIGNMENTS

RESULT 1

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O02762
ID O02762 PRELIMINARY; PRT; 56 AA.
AC O02762;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99098454; PubMed=9883985;
RA Robertson J.A., Bhattacharyya S., Ing N.H.;
RT "Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and
RT glycerinaldehyde 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";
RL J. Steroid Biochem. Mol. Biol. 67:285-292(1998).
DR EMBL; U94720; AAB57840.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 56
SQ SEQUENCE 56 AA; 6617 MW; 2AB38E08F1E8F1BC CRC64;
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Query Match 42.9%; Score 247; DB 2; Length 56;
Best Local Similarity 82.1%; Pred. No. 9.5e-14;
Matches 46; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

```
Qy      47 LDNWDSVTSTFSKLREQLGPVTQEFWDNLKETEGLRQEMSKDLEEVKAKVQPYLD 102
      |||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 LDNWDSLASTLSKVREQLGPVTQEFWDNLKETEGLRQEMSKDLEEARQKVQPYLD 56
```

RESULT 2

```
Q29248
ID Q29248 PRELIMINARY; PRT; 82 AA.
AC Q29248;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
```



```
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE.
RX MEDLINE=96128192; PubMed=8536707;
RA Hermier D., Sellier N., Rousselot-Pailley D., Forgez P.;
RT "Characterization of apolipoproteins B-100, AI and C from plasma
RT lipoprotein in the goose, Anser anser. Evidence for a genetic
RT polymorphism in ApoC-like apolipoproteins.";
RL Eur. J. Biochem. 234:586-591(1995).
DR PIR; S67972; S67972.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR Pfam; PF01442; Apolipoprotein; 1.
SQ SEQUENCE 34 AA; 3838 MW; 4BE7DFA02BF1DE91 CRC64;

Query Match 18.4%; Score 106; DB 2; Length 34;
Best Local Similarity 54.5%; Pred. No. 0.05;
Matches 18; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE 34
: |||: |||: |||: |||: : |||: |||: |||
Db 1 DEPQAPLDRLKDLVDVYLETVKASGKDYLAQFE 33

RESULT 7
APAL_ERYPA STANDARD; PRT; 20 AA.
ID APAL_ERYPA
AC P18647;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-I (Apo-AI) (Fragment).
GN Name=APOA1;
OS Erythrocebus patas (Red guenon) (Cercopithecus patas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=76184721; PubMed=178359;
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the
RT Erythrocebus patas monkey.";
RL Biochemistry 15:1928-1933(1976).
CC -!- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
CC cholesterol acyltransferase (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
DR PIR; A05313; A05313.
DR InterPro; IPR009074; Apolipo_A_E_C3.
KW Cholesterol metabolism; Direct protein sequencing; HDL;
KW Lipid transport; Plasma.
FT NON TER 20
SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 17.5%; Score 101; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 0.072;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATVYVD 20
||||: |||: |||: |||: |||:
Db 1 DEPPQTPWDRVKDLVTYYVE 20
```

```
RESULT 8
Q9QV04 PRELIMINARY; PRT; 30 AA.
ID Q9QV04
AC Q9QV04;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Apolipoprotein E (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=95355312; PubMed=7629028;
RA Motojima K., Goto S.;
RL J. Biochem. 117:597-602(1995).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
SQ SEQUENCE 30 AA; 3355 MW; 4A0103DCB6242BF3 CRC64;

Query Match 17.5%; Score 101; DB 2; Length 30;
Best Local Similarity 67.9%; Pred. No. 0.11;
Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 PQSPWDRVKDLATVYVDVLKDSGRDYVS 31
|||: |||: |||: |||: |||: |||: |||
Db 3 PQSQWDXXVXDFATVYVDVAVXDSGXDXS 30

RESULT 9
APE_SAISC STANDARD; PRT; 107 AA.
ID APE_SAISC
AC Q28995;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein E (Apo-E) (Fragment).
GN Name=APOE;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96225955; PubMed=8635577;
RA Morelli L., Wei L., Amorim A., McDermid J., Abee C.R., Frangione B.,
RA Walker L.C., Levy E.;
RT "Cerebrovascular amyloidosis in squirrel monkeys and rhesus monkeys:
RT apolipoprotein E genotype.";
RL FEBS Lett. 379:132-134(1996).
CC -!- FUNCTION: Mediates the binding, internalization, and catabolism of
CC lipoprotein particles. It can serve as a ligand for the LDL (apo
CC B/E) receptor and for the specific apo-E receptor (chylomicron
CC remnant) of hepatic tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Secreted in plasma.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U52029; AAC50442.1; -.
```



```
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245087; PubMed=7514558;
RA Tanaka T., Tsukiyama-Kohara K., Yamaguchi K., Yagi S., Tanaka S.,
RA Hasegawa A., Ohta Y., Hattori N., Kohara M.;
RT "Significance of specific antibody assay for genotyping of hepatitis C
RT virus.";
RL Hepatology 19:1347-1353(1994).
DR InterPro; IPR000745; HCV_NS4a.
DR InterPro; IPR001490; HCV_NS4b.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
FT NON TER 102_102
SQ SEQUENCE 102 AA; 11389 MW; 267CA4C1F2F7F44E CRC64;

Query Match 12.9%; Score 74.5; DB 2; Length 102;
Best Local Similarity 25.3%; Pred. No. 82;
Matches 25; Conservative 22; Mismatches 41; Indels 11; Gaps 3;

QY 9 DRVKOLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSLRQLGPVT 68
Db 12 DRDPEFATGCVSII---GRLHINQRAVVPDKVLYEAFDEMEECASRAALIEE-----G 63

QY 69 QEFWDNLEKETEGRLQEMSKOLEEVKAKVQ---PYLDDF 104
Db 64 QRIAEMLKSKIQGLLQOASKQAQDIKPAVQTSWPKVEQF 102

RESULT 13
Q6WHJ6 PRELIMINARY; PRT; 76 AA.
AC Q6WHJ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=KVP40.0307;
OS Bacteriophage KVP40.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=75320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22803260; PubMed=12923095;
RA Miller E., Lee J., Szczybinski B.;
RA Feldblyum T., White O., Paulsen I., Nierman W., Lee J.,
RA Szczybinski B., Fraser C.;
RT "Complete genome sequence of the broad-host-range vibriophage KVP40:
RT comparative genomics of a T4-related bacteriophage.";
RL J. Bacteriol. 185:5220-5233(2003).
SQ SEQUENCE 76 AA; 9023 MW; 873E2003C17C60C6 CRC64;

Query Match 12.7%; Score 73; DB 2; Length 76;
Best Local Similarity 24.3%; Pred. No. 79;
Matches 18; Conservative 12; Mismatches 24; Indels 20; Gaps 2;

QY 34 EGSALGKQLNLKLLDNWDSVTSTFSLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEV 93
Db 12 EGRGLNGFN----DNWRNAS-----LWKNIGPDAEKIKKEAEEPEEEI 51

QY 94 KAKVQPYLDDFQKK 107
Db 52 KEVKQENLEDLSER 65

RESULT 14
Q6WHJ6 PRELIMINARY; PRT; 76 AA.
AC Q6WHJ6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA2204, BAS2048; ORFNames=GBAA2204;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
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AAQ64377 PRELIMINARY; PRT; 76 AA.
AC AAQ64377;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN KVP40.0307.
OS Bacteriophage KVP40.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=75320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22803260; PubMed=12923095;
RA Miller E., Heidelberg J., Eisen J., Nelson W., Durkin A., Ciecko A.,
RA Feldblyum T., White O., Paulsen I., Nierman W., Lee J.,
RA Szczybinski B., Fraser C.;
RT "Complete genome sequence of the broad-host-range vibriophage KVP40:
RT comparative genomics of a T4-related bacteriophage.";
RL J. Bacteriol. 185:5220-5233(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Miller E., Lee J., Szczybinski B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY283928; AAQ64377.1; -.
KW Hypothetical protein.
SQ SEQUENCE 76 AA; 9023 MW; 873E2003C17C60C6 CRC64;

Query Match 12.7%; Score 73; DB 2; Length 76;
Best Local Similarity 24.3%; Pred. No. 79;
Matches 18; Conservative 12; Mismatches 24; Indels 20; Gaps 2;

QY 34 EGSALGKQLNLKLLDNWDSVTSTFSLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEV 93
Db 12 EGRGLNGFN----DNWRNAS-----LWKNIGPDAEKIKKEAEEPEEEI 51

QY 94 KAKVQPYLDDFQKK 107
Db 52 KEVKQENLEDLSER 65

RESULT 15
Q81R54 PRELIMINARY; PRT; 93 AA.
AC Q81R54; Q6HZC7; Q6KTB7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA2204, BAS2048; ORFNames=GBAA2204;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017031; AAP26082.1; -.
DR EMBL; AE017334; AAT31321.1; -.
DR EMBL; AE017225; AAT54362.1; -.
DR TIGR; BA2204; -.
KW Hypothetical protein.
SQ SEQUENCE 93 AA; 11047 MW; 1D9BD5A2B82CF5B0 CRC64;

Query Match      12.7%; Score 73; DB 2; Length 93;
Best Local Similarity 28.2%; Pred. No. 99;
Matches 20; Conservative 14; Mismatches 33; Indels 4; Gaps 1;

QY 38 LGKQLNLKLLDNWDSVTSTFSKLRQIGPVTQEFWDNLEKE----TEGLRQEMSKDLEEV 93
Db 13 LTKEQQLKVLNNEENFLGLSEAAANKSGSKSYSDWTIYKKEIEVDPKFREEMIKKEKEL 72

QY 94 KAKVQPYLDDF 104
Db 73 EMKLQKQIDDF 83
```

Search completed: December 21, 2004, 12:40:46
Job time : 197 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 12:24:32 ; Search time 152 Seconds
(without alignments)
257.247 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_133
Perfect score: 576
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LEEYKAKVQPYLDDFKKWKQ 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1158598

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|---------------------|
| 1 | 197 | 34.2 | 65 | 6 | ABP76131 | Abp76131 Human GEN |
| 2 | 162 | 28.1 | 64 | 5 | ABP31744 | Abp31744 Human apo |
| 3 | 138 | 24.0 | 42 | 2 | AAR20164 | Aar20164 Apo AI po |
| 4 | 137 | 23.8 | 26 | 7 | ADE76474 | Ade76474 ApoAI G* |
| 5 | 116 | 20.1 | 21 | 1 | AAP90956 | Aap90956 Apo AI ep |
| 6 | 112 | 19.4 | 85 | 8 | ADP87441 | Adp87441 Monkey apo |
| 7 | 110 | 19.1 | 85 | 8 | ADP87442 | Adp87442 Human apo |
| 8 | 108 | 18.8 | 22 | 1 | AAP92072 | Aap92072 Apolipop |
| 9 | 108 | 18.8 | 84 | 2 | AAY42554 | Aay42554 Apolipop |
| 10 | 108 | 18.8 | 85 | 8 | ADP87440 | Adp87440 Baboon ap |
| 11 | 104 | 18.1 | 85 | 8 | ADP87439 | Adp87439 pig apoli |
| 12 | 101 | 17.5 | 85 | 8 | ADP87438 | Adp87438 Chicken a |
| 13 | 97 | 16.8 | 19 | 1 | AAP92073 | Aap92073 Apolipop |
| 14 | 96.5 | 16.8 | 95 | 6 | ABP70773 | Abp70773 Human apo |
| 15 | 95 | 16.5 | 107 | 8 | ADP87432 | Adp87432 Rat apoli |
| 16 | 95 | 16.5 | 107 | 8 | ADP87431 | Adp87431 Rat apoli |
| 17 | 94 | 16.3 | 30 | 7 | ADC29665 | Adc29665 Antioxi |
| 18 | 94 | 16.3 | 30 | 7 | ADC29666 | Adc29666 Antioxi |
| 19 | 92 | 16.0 | 18 | 7 | ADC29658 | Adc29658 Antioxi |
| 20 | 91 | 15.8 | 16 | 2 | AAY27065 | Aay27065 Peptide S |
| 21 | 89 | 15.5 | 16 | 6 | ABP57175 | Abp57175 Breast ca |
| 22 | 89 | 15.5 | 30 | 7 | ADC29668 | Adc29668 Antioxi |
| 23 | 89 | 15.5 | 30 | 7 | ADC29664 | Adc29664 Antioxi |
| 24 | 87 | 15.1 | 17 | 8 | ADH35704 | Adh35704 Apolipop |
| 25 | 87 | 15.1 | 17 | 8 | ADH35715 | Adh35715 Apolipop |

| | | | | | | |
|----|----|------|----|---|----------|--------------------|
| 26 | 87 | 15.1 | 18 | 7 | ADC29657 | Adc29657 Antioxi |
| 27 | 87 | 15.1 | 18 | 7 | ADC29660 | Adc29660 Antioxi |
| 28 | 86 | 14.9 | 30 | 7 | ADC29667 | Adc29667 Antioxi |
| 29 | 86 | 14.9 | 30 | 7 | ADC29671 | Adc29671 Antioxi |
| 30 | 85 | 14.8 | 30 | 7 | ADC29669 | Adc29669 Antioxi |
| 31 | 85 | 14.8 | 30 | 7 | ADC29670 | Adc29670 Antioxi |
| 32 | 84 | 14.6 | 18 | 7 | ADC29663 | Adc29663 Antioxi |
| 33 | 84 | 14.6 | 18 | 7 | ADC29659 | Adc29659 Antioxi |
| 34 | 84 | 14.6 | 96 | 8 | ADP87419 | Adp87419 Tupala gl |
| 35 | 83 | 14.4 | 18 | 7 | ADC29662 | Adc29662 Antioxi |
| 36 | 83 | 14.4 | 18 | 7 | ADC29661 | Adc29661 Antioxi |
| 37 | 83 | 14.4 | 32 | 2 | AAR20165 | Aar20165 Apo AI po |
| 38 | 83 | 14.4 | 96 | 8 | ADP87420 | Adp87420 Squirrel |
| 39 | 82 | 14.2 | 96 | 8 | ADP87422 | Adp87422 Baboon ap |
| 40 | 82 | 14.2 | 96 | 8 | ADP87423 | Adp87423 Rhesus ma |
| 41 | 82 | 14.2 | 96 | 8 | ADP87421 | Adp87421 Monkey ap |
| 42 | 81 | 14.1 | 16 | 2 | AAR72706 | Aar72706 Human apo |
| 43 | 81 | 14.1 | 16 | 2 | AAR34033 | Aar34033 Sequence |
| 44 | 80 | 13.9 | 16 | 4 | AAG62607 | Aag62607 Apolipop |
| 45 | 79 | 13.7 | 96 | 8 | ADP87430 | Adp87430 Gorilla a |

ALIGNMENTS

RESULT 1
ABP76131
ID ABP76131 standard; protein; 65 AA.

XX AC ABP76131;

XX DT 21-FEB-2003 (first entry)

XX DE Human GENSET protein SEQ ID 457.

KW Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiand;
KW gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;
KW inflammatory disease; immune disorder; neuromuscular; toxicity;
KW central nervous system; cardiovascular; gastrointestinal.

XX OS Homo sapiens.

XX PN WO200283898-A1.

XX PD 24-OCT-2002.

XX PF 18-APR-2001; 2001WO-IB000914.

XX PR 18-APR-2001; 2001WO-IB000914.

XX PA (GEST) GENSET.

XX PI Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;
XX DR WPI; 2003-075548/07.

XX PT New GENSET polynucleotides and polypeptides, useful for treating heavy
PT metal toxicity, cancer, inflammatory diseases, immune disorders, and the
PT neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
PT toxicity.

XX PS Claim 14; Page 535; 735pp; English.

XX CC The present invention relates to novel GENSET polynucleotides (ABZ36404-
CC ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides
CC and polypeptides are useful in screening and diagnostic assays for
CC abnormal GENSET expression and/or biological activity. They are also
CC useful for screening of compounds for treating or preventing GENSET-
CC related disorders, such as heavy metal toxicity, cancer, inflammatory
CC diseases, immune disorders, and the neuromuscular, central nervous system
CC (CNS), cardiovascular or gastrointestinal effects of the toxicity

XX SQ Sequence 65 AA;

PS Claim 2; Page 68; 87pp; English.

XX The peptides represented in AAR20164-65 are capable of immunologically

CC mimicking an Apo AI epitope. They are useful in diagnosis and detection

CC of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is

CC useful in therapeutic methods for increasing LCAT- mediated cholesterol

CC esterification in humans. The Apo AI polypeptide is selected from the

CC peptides indicated in the features and includes amino acids 13-28

CC defining a conserved native epitope on Apo AI capable of immunoreacting

CC with monoclonal antibody MAB AI-11. (Updated on 25-MAR-2003 to correct PA

CC field.)

XX

SQ Sequence 42 AA;

Query Match 24.0%; Score 138; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 3.7e-06;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 QEMSKDLEEVKAKVQPYLDDFQKKWQ 109

Db 1 QEMSKDLEEVKAKVQPYLDDFQKKWQ 26

RESULT 4

ADE76474

ID ADE76474 standard; peptide; 26 AA.

XX

AC ADE76474;

XX

DT 29-JAN-2004 (first entry)

XX

DE ApoAI G* amphipathic helical domain-derived peptide - SEQ ID 21.

XX

KW G-type; atherosclerosis; inflammatory; G* amphipathic helix;

KW antiarteriosclerotic; antirheumatic; antiarthritic; immunosuppressive;

KW dermatological; antiinflammatory; osteopathic; neuroprotective;

KW nootropic; anti-HIV; virucide; antibacterial; rheumatoid arthritis;

KW systemic lupus erythematosus; polyarteritis nodosa; osteoporosis;

KW Alzheimer's disease; AIDS; infection; apoAI.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 1. .26 /note= "Optionally D-form residue"

FT Modified-site 1 /note= "Optional N-terminal acetyl"

FT Modified-site 26 /note= "Optional C-terminal amide"

XX

PN US2003191057-A1.

XX

PD 09-OCT-2003.

XX

PF 05-APR-2002; 2002US-00120508.

XX

PR 05-APR-2002; 2002US-00120508.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Fogelman AM, Navab M;

XX

XX WPI; 2003-831662/77.

DR

XX

PT New G-type polypeptides for preventing or ameliorating symptoms of

PT atherosclerosis or pathologies associated with an inflammatory responses

PT e.g. rheumatoid arthritis, osteoporosis, Alzheimer's disease, AIDS or

PT infections.

XX

PS Claim 7; SEQ ID NO 21; 29pp; English.

XX

CC The invention relates to a novel isolated G-type polypeptide that

CC ameliorates a symptom of atherosclerosis or other pathology associated

CC with an inflammatory response comprising an amphipathic helical peptide

CC having charged residues on the polar face of the peptide and possessing a

CC wide non-polar face. The polypeptide of the invention demonstrates

CC antiarteriosclerotic, antirheumatic, antiarthritic, immunosuppressive,

CC dermatological, antiinflammatory, osteopathic, neuroprotective,

CC nootropic, anti-HIV, virucide and antibacterial activities. The

CC composition and methods of the invention may be useful in preventing or

CC ameliorating one or more symptoms of atherosclerosis and/or pathologies

CC characterised by an inflammatory response such as rheumatoid arthritis,

CC systemic lupus erythematosus, polyarteritis nodosa, osteoporosis,

CC Alzheimer's disease, AIDS or infection. The current sequence is that of

CC the apoAI G* amphipathic helical domain-derived peptide of the invention.

XX

SQ Sequence 26 AA;

Query Match 23.8%; Score 137; DB 7; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WDRVKDLATVYVDVLKDSGRDYVSQF 33

Db 1 WDRVKDLATVYVDVLKDSGRDYVSQF 26

RESULT 5

AAP90956

ID AAP90956 standard; peptide; 21 AA.

XX

AC AAP90956;

XX

DT 25-MAR-2003 (revised)

DT 19-FEB-1990 (first entry)

XX

DE Apo AI epitope.

XX

KW High density lipoproteins.

XX

OS Synthetic.

XX

PN WO8909403-A.

XX

PD 05-OCT-1989.

XX

PF 27-MAR-1989; 89WO-US001262.

XX

PR 29-MAR-1988; 88US-00174698.

XX

PA (SCRI) SCRIPPS CLINIC & RES FOUND.

XX

PI Curtiss LK, Smith RS;

XX

DR WPI; 1989-309644/42.

XX

PT Apo lipoprotein peptide and monoclonal antibody against it - used to

PT assay peptide in vascular fluid to identify risk of coronary artery

PT disease.

XX

PS Claim 2; Page 41; 49pp; English.

XX

CC Apo AI contains the sequence below (Claim 1 claims AAs 1-15). There is an

CC inverse correlation between plasma levels of Apo AI and coronary artery

CC disease risk. The monoclonal antibody recognises this epitope on native

CC Apo AI. (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 21 AA;

Query Match 20.1%; Score 116; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATVYVDV 21

Db 1 DEPPQSPWDRVKDLATVYVDV 21


```

RESULT 6
ADP87441
ID ADP87441 standard; protein; 85 AA.
XX
AC ADP87441;
XX
DT 09-SEP-2004 (first entry)
XX
DE Monkey apolipoprotein A (APO-A) precursor protein.
XX
KW Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW monkey.
XX
OS Macaca fascicularis.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX
DR WPI; 2004-480967/45.
XX
PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 48; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recogniser and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC monkey apolipoprotein A (APO-A) IV precursor protein. This sequence is
CC used to illustrate the method of the invention.
XX
SQ Sequence 85 AA;

Query Match 19.4%; Score 112; DB 8; Length 85;
Best Local Similarity 33.3%; Pred. No. 0.0031;
Matches 24; Conservative 19; Mismatches 29; Indels 0; Gaps 0;

QY 36 SALGKQLNLKLLDNWDSVTSTFTSKLREQLGVPVTQEFWDNLEKETEGLRQEMSKOLEEVKA 95
Db 1 SELTQQLNALFQDKLGEVNTYAGDLQKKLVFPFATELHERLAKDSEKIKEIRKELEVRA 60

QY 96 KVQPYLDDFQKK 107
Db 61 RLLPHANEVSQK 72

RESULT 7
ADP87442
ID ADP87442 standard; protein; 85 AA.
XX
AC ADP87442;
XX
```

```

XX 09-SEP-2004 (first entry)
DT Human apolipoprotein A (APO-A) precursor protein.
XX
DE Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX
DR WPI; 2004-480967/45.
XX
PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 49; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recogniser and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC human apolipoprotein A (APO-A) IV precursor protein. This sequence is
CC used to illustrate the method of the invention.
XX
SQ Sequence 85 AA;

Query Match 19.1%; Score 110; DB 8; Length 85;
Best Local Similarity 31.9%; Pred. No. 0.0049;
Matches 23; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 36 SALGKQLNLKLLDNWDSVTSTFTSKLREQLGVPVTQEFWDNLEKETEGLRQEMSKOLEEVKA 95
Db 1 SELTQQLNALFQDKLGEVNTYAGDLQKKLVFPFATELHERLAKDSEKIKEEIGKELEELRA 60

QY 96 KVQPYLDDFQKK 107
Db 61 RLLPHANEVSQK 72

RESULT 8
AAP92072
ID AAP92072 standard; peptide; 22 AA.
XX
AC AAP92072;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 10-APR-1990 (first entry)
XX
DE Apolipoprotein AI (Apo AI) polypeptide.
XX
```


XX 09-SEP-2004 (first entry)
DT
XX
DE Baboon apolipoprotein A (APO-A) IV precursor protein.
XX
KW Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW baboon.
XX
OS Papio anubis.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX
DR WPI; 2004-480967/45.
XX
PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 47; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recogniser and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC baboon apolipoprotein A (APO-A) IV precursor protein. This sequence is
CC used to illustrate the method of the invention.
XX
SQ Sequence 85 AA;

Query Match 18.8%; Score 108; DB 8; Length 85;
Best Local Similarity 31.9%; Pred. No. 0.0077;
Matches 23; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 36 SALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKA 95
Db 1 SELTQQLNALFQDKLGEVNTYAGDLQKKLVFPFATELHERLAKDSKKLKEEIRKELEEVRA 60

QY 96 KVQPYLDDFQKK 107
Db 61 RLLPHANEVSQK 72

RESULT 11
ADP87439
ID ADP87439 standard; protein; 85 AA.
XX
AC ADP87439;
XX
DT 09-SEP-2004 (first entry)
XX
DE Pig apolipoprotein A (APO-A) IV precursor protein.
XX
KW Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;

KW pig.
XX
OS Sus scrofa.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX
DR WPI; 2004-480967/45.
XX
PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 46; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recogniser and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is pig
CC apolipoprotein A (APO-A) IV precursor protein. This sequence is used to
CC illustrate the method of the invention.
XX
SQ Sequence 85 AA;

Query Match 18.1%; Score 104; DB 8; Length 85;
Best Local Similarity 30.6%; Pred. No. 0.019;
Matches 22; Conservative 20; Mismatches 30; Indels 0; Gaps 0;

QY 36 SALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKA 95
Db 1 SELTQQLNTLTFQDKLGEVNTYTEDLQKKLVFPFATELHERLTKDSEKLEEIRLEELRA 60

QY 96 KVQPYLDDFQKK 107
Db 61 RLLPHATEVSQK 72

RESULT 12
ADP87438
ID ADP87438 standard; protein; 85 AA.
XX
AC ADP87438;
XX
DT 09-SEP-2004 (first entry)
XX
DE Chicken apolipoprotein A (APO-A) IV protein.
XX
KW Browseable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW chicken.
XX
OS Gallus gallus.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.

```
XX PF 09-DEC-2003; 2003WO-US038935.
XX PR 09-DEC-2002; 2002US-0431879P.
XX PA (APPL-) APPLERA CORP.
XX PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;
XX DR WPI; 2004-480967/45.
XX PT Browsable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptor, a recognizer, and
PT an output.
XX PS Disclosure; SEQ ID NO 45; 113pp; English.
XX CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptor, a recognizer and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC chicken apolipoprotein A (APO-A) IV protein. This sequence is used to
CC illustrate the method of the invention.
XX SQ Sequence 85 AA;
Query Match 17.5%; Score 101; DB 8; Length 85;
Best Local Similarity 30.9%; Pred. No. 0.037;
Matches 21; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
QY 40 KQLNLKLLDNWDSVTSTFSLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQP 99
Db 5 KQLNTLLQSNLQNSANSYAEELQRRLLVPFATELQAQLVQDSQRLKKIQBELAELQAKLAP 64
QY 100 YLDDFQKK 107
Db 65 YAEVHQH 72
RESULT 13
AAP92073
ID AAP92073 standard; peptide; 19 AA.
XX AC AAP92073;
XX DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 10-APR-1990 (first entry)
XX DE Apolipoprotein AI (Apo AI) polypeptide.
XX KW Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL;
KW coronary artery disease; CAD; Apo AI epitope; AI87-105.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..15
FT /label= AI87-101
FT Peptide 4..19
FT /label= AI90-105
FT Peptide 7..15
FT /label= AI93-101
FT Peptide 9..19
FT /label= AI95-105
```

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XX PN WO8904486-A.
XX PD 18-MAY-1989.
XX PF 02-NOV-1988; 88WO-US003903.
XX PR 03-NOV-1987; 87US-00116248.
XX PA (SCRI ) SCRIPPS CLINIC & RES FOUND.
XX PI Curtiss LK, Smith RR;
XX DR WPI; 1989-165740/22.
XX PT New monoclonal antibody and polypeptide antigens - directed against APO
PT AI-HDL epitope, useful in diagnostic assays.
XX PS Claim 2; Table 1-2; 62pp; English.
XX CC AI87-105 and smaller peptides contained within this sequence - see FT.
CC Such Apo AI peptides are capable of immunologically mimicking a native
CC conserved Apo AI epitope. They may be helpful in the diagnosis of risk of
CC coronary heart disease. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX SQ Sequence 19 AA;
Query Match 16.8%; Score 97; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 SKDLEEVKAKVQPYLDDFQ 105
Db 1 SKDLEEVKAKVQPYLDDFQ 19
RESULT 14
ABP70773
ID ABP70773 standard; protein; 95 AA.
XX AC ABP70773;
XX DT 23-MAY-2003 (first entry)
XX DE Human apolipoprotein AIV related protein, AA4RP, peptide.
XX KW Human; hypolipemic; Apolipoprotein AIV Related Protein; AA4RP;
KW lipid metabolism; cardiovascular disease; hyperlipidemia;
KW coronary disease.
XX OS Homo sapiens.
XX PN WO2003023408-A1.
XX PD 20-MAR-2003.
XX PF 06-SEP-2002; 2002WO-FR003041.
XX PR 07-SEP-2001; 2001FR-00011598.
PR 12-AUG-2002; 2002FR-00010205.
XX PA (GENF-) GENFIT.
XX PI Najib J, Majd Z;
XX DR WPI; 2003-301101/29.
XX PT New synthetic peptide from apolipoprotein AIV related protein, useful for
PT raising antibodies, used for diagnosis and treatment of disorders of
PT lipid metabolism.
XX
```

PS Claim 1; Page 6; 45pp; French.

XX The present sequence is a peptide fragment of human Apolipoprotein AIV
CC Related Protein (AA4RP). The peptide fragment is useful for raising
CC specific antibodies (Ab) against AA4RP, so are useful in immunoassays for
CC detecting or determining AA4RP, especially to identify subjects at risk
CC of developing disorders of lipid metabolism (particularly cardiovascular
CC diseases associated with hyperlipidemia, e.g. coronary disease). Ab are
CC also useful for protein purification and, optionally when conjugated to a
CC toxin or pharmaceutical, for treating the specified diseases

XX Sequence 95 AA;

SQ Query Match 16.8%; Score 96.5; DB 6; Length 95;
 Best Local Similarity 29.5%; Pred. No. 0.12;
Matches 23; Conservative 21; Mismatches 31; Indels 3; Gaps 2;

QY 24 DSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGLR 83
 | | | | | : : : | | : : : | | : : : | | : : : | | : : : | : |
 :
Db 18 DKGR--VEQIHQOKWARE-PATLKDSLEQDLNNMNKFLKLRPLSGSEAPRLPQDPVGM 74

QY 84 QEMSKDLEEVKAKVQPYL 101
 :
Db 75 RQLQEELEEVKARLQPYM 92

RESULT 15

ADP87432

ID ADP87432 standard; protein; 107 AA.

XX

AC ADP87432;

XX

DT 09-SEP-2004 (first entry)

XX

DE Rat apolipoprotein C (APO-C) IV protein.

XX

KW Browseable database system; ontology; protein analysis;

KW Gene product classification; genomic analysis; apolipoprotein C; APO-C;

KW Rat.

XX

OS Rattus norvegicus.

XX

PN WO2004053769-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-US038935.

XX

PR 09-DEC-2002; 2002US-0431879P.

XX

PA (APPL-) APPLERA CORP.

XX

PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;

PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;

PI Doremieux O;

XX

DR WPI; 2004-480967/45.

XX

PT Browseable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.

XX

PS Disclosure; SEQ ID NO 39; 113pp; English.

XX

CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recognizer and an output.
CC The invention also provides a method of operation for use with a
CC browseable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and

CC in facilitating comparative genomic analysis. The present sequence is rat
CC apolipoprotein C (APO-C) IV protein. This sequence is used to illustrate
CC the method of the invention.

XX

SQ Sequence 107 AA;

 Query Match 16.5%; Score 95; DB 8; Length 107;
 Best Local Similarity 29.3%; Pred. No. 0.19;
Matches 22; Conservative 18; Mismatches 27; Indels 8; Gaps 1;

QY 40 KQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQP 99
 : | | | | : : : | | : : : | | : : : | | : : : | | : : : | : |
Db 5 QQLNTLTFQDKLGNINTYADDLQNKLVPPFAVQLSGHLTKETERVREEIQKELEDLRANMMP 64

QY 100 YL-----DDFOK 106
 : | : | |
Db 65 HANKVSMFGDNVQK 79

Search completed: December 21, 2004, 12:37:24

Job time : 156 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 21, 2004, 12:14:35 ; Search time 144 Seconds
(without alignments)
270.861 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_133
Perfect score: 576
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LSEVKAKVQPYLDDFQKKWQ 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1589859 seqs, 357834939 residues
Total number of hits satisfying chosen parameters: 739951

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA: *
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length DB | ID | Description |
|------------|-------|---------------|-----------|----|---------------------------------------|
| 1 | 332.5 | 57.7 | 93 | 15 | US-10-038-854-403 Sequence 403, App |
| 2 | 332.5 | 57.7 | 93 | 15 | US-10-038-854-405 Sequence 405, App |
| 3 | 318 | 55.2 | 86 | 15 | US-10-424-599-276814 Sequence 276814, |
| 4 | 227 | 39.4 | 43 | 15 | US-10-465-789A-89 Sequence 89, Appl |
| 5 | 162 | 28.1 | 64 | 11 | US-09-864-408A-1434 Sequence 1434, Ap |
| 6 | 137 | 23.8 | 26 | 14 | US-10-120-508-21 Sequence 21, Appl |
| 7 | 118 | 20.5 | 22 | 15 | US-10-465-789A-50 Sequence 50, Appl |
| 8 | 112 | 19.4 | 22 | 15 | US-10-465-789A-49 Sequence 49, Appl |
| 9 | 96.5 | 16.8 | 95 | 17 | US-10-487-096-2 Sequence 2, Appli |
| 10 | 94 | 16.3 | 30 | 14 | US-10-142-238A-40 Sequence 40, Appl |
| 11 | 94 | 16.3 | 30 | 14 | US-10-142-238A-41 Sequence 41, Appl |
| 12 | 92 | 16.0 | 18 | 14 | US-10-142-238A-33 Sequence 33, Appl |
| 13 | 89 | 15.5 | 16 | 17 | US-10-700-340-37 Sequence 37, Appl |

| | | | | | | |
|----|------|------|-----|----|----------------------|-------------------|
| 14 | 89 | 15.5 | 30 | 14 | US-10-142-238A-39 | Sequence 39, Appl |
| 15 | 89 | 15.5 | 30 | 14 | US-10-142-238A-43 | Sequence 43, Appl |
| 16 | 87 | 15.1 | 17 | 15 | US-10-601-100-44 | Sequence 44, Appl |
| 17 | 87 | 15.1 | 18 | 14 | US-10-142-238A-32 | Sequence 32, Appl |
| 18 | 87 | 15.1 | 18 | 14 | US-10-142-238A-35 | Sequence 35, Appl |
| 19 | 86 | 14.9 | 30 | 14 | US-10-142-238A-42 | Sequence 42, Appl |
| 20 | 86 | 14.9 | 30 | 14 | US-10-142-238A-46 | Sequence 46, Appl |
| 21 | 85 | 14.8 | 30 | 14 | US-10-142-238A-44 | Sequence 44, Appl |
| 22 | 85 | 14.8 | 30 | 14 | US-10-142-238A-45 | Sequence 45, Appl |
| 23 | 84 | 14.6 | 18 | 14 | US-10-142-238A-34 | Sequence 34, Appl |
| 24 | 84 | 14.6 | 18 | 14 | US-10-142-238A-38 | Sequence 38, Appl |
| 25 | 83 | 14.4 | 18 | 14 | US-10-142-238A-36 | Sequence 36, Appl |
| 26 | 83 | 14.4 | 18 | 14 | US-10-142-238A-37 | Sequence 37, Appl |
| 27 | 74 | 12.8 | 14 | 15 | US-10-601-100-43 | Sequence 43, Appl |
| 28 | 67.5 | 11.7 | 72 | 16 | US-10-767-701-37365 | Sequence 37365, A |
| 29 | 67 | 11.6 | 21 | 14 | US-10-076-047A-34 | Sequence 34, Appl |
| 30 | 67 | 11.6 | 22 | 15 | US-10-465-789A-52 | Sequence 52, Appl |
| 31 | 66 | 11.5 | 13 | 14 | US-10-014-340-123 | Sequence 123, App |
| 32 | 66 | 11.5 | 13 | 15 | US-10-264-309-76 | Sequence 76, Appl |
| 33 | 66 | 11.5 | 13 | 15 | US-10-601-100-36 | Sequence 36, Appl |
| 34 | 65.5 | 11.4 | 99 | 15 | US-10-674-755-16 | Sequence 16, Appl |
| 35 | 64 | 11.1 | 62 | 9 | US-09-864-761-40424 | Sequence 40424, A |
| 36 | 63 | 10.9 | 10 | 14 | US-10-033-741-11 | Sequence 11, Appl |
| 37 | 63 | 10.9 | 10 | 14 | US-10-014-340-79 | Sequence 79, Appl |
| 38 | 63 | 10.9 | 10 | 15 | US-10-264-309-52 | Sequence 52, Appl |
| 39 | 63 | 10.9 | 10 | 15 | US-10-601-100-55 | Sequence 55, Appl |
| 40 | 63 | 10.9 | 10 | 17 | US-10-700-340-21 | Sequence 21, Appl |
| 41 | 62.5 | 10.9 | 97 | 17 | US-10-425-115-300637 | Sequence 300637, |
| 42 | 62 | 10.8 | 80 | 15 | US-10-424-599-197965 | Sequence 197965, |
| 43 | 62 | 10.8 | 108 | 15 | US-10-424-599-243777 | Sequence 243777, |
| 44 | 61.5 | 10.7 | 99 | 15 | US-10-674-755-11 | Sequence 11, Appl |
| 45 | 61 | 10.6 | 100 | 15 | US-10-674-755-12 | Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-10-038-854-403
; Sequence 403, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22

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; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 403
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-403

Query Match      57.7%; Score 332.5; DB 15; Length 93;
Best Local Similarity 71.9%; Pred. No. 4e-25;
Matches 69; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY      14 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 73
      |||||||
Db      1 LATVYVDVLK-----DSVTSTFSKLREQLGPVTQEFWD 33

QY      74 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 109
      |||||||
Db      34 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 69

RESULT 2
US-10-038-854-405
; Sequence 405, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
```

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; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 405
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-405

Query Match      57.7%; Score 332.5; DB 15; Length 93;
Best Local Similarity 71.9%; Pred. No. 4e-25;
Matches 69; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY      14 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 73
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Db      1 LATVYVDVLK-----DSVTSTFSKLREQLGPVTQEFWD 33

QY      74 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 109
      |||||||
Db      34 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 69

RESULT 3
US-10-424-599-276814
; Sequence 276814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276814
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91983C.1.pap
US-10-424-599-276814

Query Match      55.2%; Score 318; DB 15; Length 86;
Best Local Similarity 98.4%; Pred. No. 9.8e-24;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 8
US-10-465-789A-49
; Sequence 49, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 1
US-10-465-789A-49

Query Match          19.4%; Score 112; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 LKLLDNWDSVTFSKLRQLG 65
| | | | | | | | | | | | | | | | | |
Db 1 LKLLDNWDSVTFSKLRQLG 22

RESULT 9
US-10-487-096-2
; Sequence 2, Application US/10487096
; Publication No. US20040197823A1
; GENERAL INFORMATION:
; APPLICANT: GENFIT SA
; TITLE OF INVENTION: Compositions and Methods for the assay of AA4RP
; FILE REFERENCE: B0157W0
; CURRENT APPLICATION NUMBER: US/10/487,096
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence : synthetic peptide AA4RP
US-10-487-096-2

Query Match          16.8%; Score 96.5; DB 17; Length 95;
Best Local Similarity 29.5%; Pred. No. 0.081;
Matches 23; Conservative 21; Mismatches 31; Indels 3; Gaps 2;

QY 24 DSGRDYVSQFEGSALGKQLNLKLLDNWDSVTFSKLRQLGPVTQEFWDNLEKETEGLR 83
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18 DKGR--VEQIHQQKWARE-PATLKDSLEQDLNNMNKFKLEKRLPLSGSEAPRLPQDPVGMR 74

QY 84 QEMSKDLEEVKAKVQPYL 101
::: ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 RQLQEELEEVEVKARLQPYM 92

RESULT 10
US-10-142-238A-40
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; Sequence 40, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-40

Query Match          16.3%; Score 94; DB 14; Length 30;
Best Local Similarity 95.0%; Pred. No. 0.034;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 LNLKLLDNWDSVTSTFSKLR 61
| | | | | | | | | | | | | | | | | |
Db 11 LPLKLLDNWDSVTSTFSKLR 30

RESULT 11
US-10-142-238A-41
; Sequence 41, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 30
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-41

Query Match          16.3%; Score 94; DB 14; Length 30;
Best Local Similarity 95.0%; Pred. No. 0.034;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 LNLKLLDNWDSVTSTFSKLR 61
| | | | | | | | | | | | | | | | | |
Db 11 LPLKLLDNWDSVTSTFSKLR 30

RESULT 12
US-10-142-238A-33
; Sequence 33, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
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; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-33

Query Match 16.0%; Score 92; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 LKLLDNWDSVTSTFSKLR 61
| | | | | | | | | | | | | | | |
Db 1 LKLLDNWDSVTSTFSKLR 18

RESULT 13
US-10-700-340-37
; Sequence 37, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREAST CANCER
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-37

Query Match 15.5%; Score 89; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EQLGPVTQEFWDNLEK 77
| | | | | | | | | | | | | | | |
Db 1 EQLGPVTQEFWDNLEK 16

RESULT 14
US-10-142-238A-39
; Sequence 39, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A

; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-39

Query Match 15.5%; Score 89; DB 14; Length 30;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 42 LNLKLLDNWDSVTSTFSKLR 61
| | | | | | | | | | | | | | | |
Db 11 LPLKCLDNWDSVTSTFSKLR 30

RESULT 15
US-10-142-238A-43
; Sequence 43, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 30
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-43

Query Match 15.5%; Score 89; DB 14; Length 30;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 42 LNLKLLDNWDSVTSTFSKLR 61
| | | | | | | | | | | | | | | |
Db 11 LPLKCLDNWDSVTSTFSKLR 30

Search completed: December 21, 2004, 12:24:19
Job time : 145 secs

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| Matches 22; Conservative 21; Mismatches 31; Indels 18; Gaps 3; | |
| QY | 10 RVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRQLGPTVQ 69 : : : : : : : : : : : : : : : |
| Db | 24 KISDLAQI-LDVHRTASNIVN--NSSRITLEMAVKLAKVFDT-----TP 65 |
| QY | 70 EFDWNLEKETETGLRQEMSKDLEEVKAKVQPYL 101 : : : : : : : : : : : : : |
| Db | 66 EFWLNLQTRIDLWDLEHNKRFQQSLANVKPAL 97 |
| RESULT 8 | |
| I68742 | |
| integral membrane protein - rat (fragment) | |
| C;Species: Rattus norvegicus (Norway rat) | |
| C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004 | |
| C;Accession: I68742 | |
| R;Chao, N.J.; Timmerman, L.; McDevitt, H.O.; Jacob, C.O. | |
| Immunogenetics 29, 231-234, 1989 | |
| A;Title: molecular characterization of mhc class ii antigens (beta-1 domains) in the bb | |
| A;Reference number: I54455; MUID:89197303; PMID:2784784 | |
| A;Accession: I68742 | |
| A;Status: preliminary; translated from GB/EMBL/DBJ | |
| A;Molecule type: mRNA | |
| A;Residues: 1-96 <RES> | |
| A;Cross-references: UNIPROT:Q31284; GB:M24932; NID:g205427; PIDN:AAA41605.1; PID:g205428 | |
| C;Genetics: | |
| A;Gene: RT1.B | |
| C;Superfamily: class II histocompatibility antigen; immunoglobulin homology | |
| Query Match 10.7%; Score 61.5; DB 2; Length 96; | |
| Best Local Similarity 29.5%; Pred. No. 1.6e+02; | |
| Matches 23; Conservative 12; Mismatches 28; Indels 15; Gaps 4; | |
| QY | 23 KDSGRDYVSQFEGS---ALGKQ-----LNLKLLDNWDSVTSTFSKLRQLGPTVQE 70 : : : : : : : : : : : : : : : |
| Db | 1 RDSPRDFVYQFEGQCYTTGTQRMRLVTRHIYNREYVRFDSDLGEYRALTE-LGRPSAE 59 |
| QY | 71 FWDNLEKETETGLRQEMSK 88 : : : : : : |
| Db | 60 YWN--KQYLEQTRAELDR 75 |
| RESULT 9 | |
| C90225 | |
| hypothetical protein SSO6469 [imported] - Sulfolobus solfataricus | |
| C;Species: Sulfolobus solfataricus | |
| C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 | |
| C;Accession: C90225 | |
| R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan- | |
| Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F | |
| arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. | |
| submitted to GenBank, April 2001 | |
| A;Description: Sulfolobus solfataricus complete genome. | |
| A;Reference number: A99139 | |
| A;Accession: C90225 | |
| A;Status: preliminary | |
| A;Molecule type: DNA | |
| A;Residues: 1-75 <KUR> | |
| A;Cross-references: UNIPROT:Q97ZP8; GB:AE006641; NID:g13813934; PIDN:AAK41058.1; GSPDB:G | |
| C;Genetics: | |
| A;Gene: SSO6469 | |
| Query Match 10.6%; Score 61; DB 2; Length 75; | |
| Best Local Similarity 21.8%; Pred. No. 1.3e+02; | |
| Matches 22; Conservative 17; Mismatches 20; Indels 42; Gaps 3; | |
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| Db | 12 PDEELWKIIVDEAEKRKVSVY-EVLKDAFNCYIREKGNKVSMEEIVKEL----- 60 |
| QY | 58 SKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVQ 98 : : : : |

| | |
|--|--|
| Db | 61 -----QELKKRVEELEKKVK 75 |
| RESULT 10 | |
| C90342 | |
| hypothetical protein SSO8938 [imported] - Sulfolobus solfataricus | |
| C;Species: Sulfolobus solfataricus | |
| C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 | |
| C;Accession: C90342 | |
| R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan | |
| Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, | |
| arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. | |
| submitted to GenBank, April 2001 | |
| A;Description: Sulfolobus solfataricus complete genome. | |
| A;Reference number: A99139 | |
| A;Accession: C90342 | |
| A;Status: preliminary | |
| A;Molecule type: DNA | |
| A;Residues: 1-75 <KUR> | |
| A;Cross-references: UNIPROT:Q97XE7; GB:AE006641; NID:g13815050; PIDN:AAK41994.1; GSPDB:A | |
| C;Genetics: | |
| A;Gene: SSO8938 | |
| Query Match 10.6%; Score 61; DB 2; Length 75; | |
| Best Local Similarity 22.8%; Pred. No. 1.3e+02; | |
| Matches 23; Conservative 18; Mismatches 18; Indels 42; Gaps 4; | |
| QY | 3 PPQSPWDRVKDLA-----TVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTF 57 : : : : : : : : : : : : : : : : : |
| Db | 12 PDEELWKIIVDEAEKRKVSVY-EVLKDAFECYMKKEGNKI----- 51 |
| QY | 58 SKLREQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVQ 98 : : : : : : : : |
| Db | 52 -----SLEEVNKL-QELKKRVEELEKKVK 75 |
| RESULT 11 | |
| A59010 | |
| antifreeze protein LS-12 - longhorn sculpin | |
| C;Species: Myoxocephalus octodecimspinosus (longhorn sculpin) | |
| C;Date: 10-Oct-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004 | |
| C;Accession: A59010 | |
| R;Deng, G.; Andrews, D.W.; Laursen, R.A. | |
| FEBS Lett. 402, 17-20, 1997 | |
| A;Reference number: A59010; MUID:97165956; PMID:9013849 | |
| A;Accession: A59010 | |
| A;Status: preliminary | |
| A;Molecule type: protein | |
| A;Residues: 1-108 <LAU> | |
| A;Cross-references: UNIPROT:P80961 | |
| A;Experimental source: blood plasma | |
| C;Keywords: antifreeze; plasma; pyroglutamic acid | |
| F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental | |
| Query Match 10.6%; Score 61; DB 2; Length 108; | |
| Best Local Similarity 22.4%; Pred. No. 2e+02; | |
| Matches 11; Conservative 16; Mismatches 22; Indels 0; Gaps 0; | |
| QY | 61 REQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 109 : : : : : : : : : : : : : : : |
| Db | 45 KTQLQPLVAQIQEQMKTATNVEEQIRPLTANVQAHLQPQIDNFKQME 93 |
| RESULT 12 | |
| F71511 | |
| hypothetical protein Cr466 - Chlamydia trachomatis (serotype D, strain UW3/Cx) | |
| C;Species: Chlamydia trachomatis | |
| C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004 | |
| C;Accession: F71511 | |
| R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell | |
| Science 282, 754-759, 1998 | |
| A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra | |
| A;Reference number: A71570; MUID:99000809; PMID:9784136 | |

A;Accession: F71511
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <ARN>
A;Cross-references: UNIPROT:O84472; GB:AE001320; GB:AE001273; NID:g3328891; PIDN:AAC6806
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT466
C;Superfamily: conserved hypothetical protein CP0165

Query Match 10.6%; Score 61; DB 2; Length 109;
Best Local Similarity 25.3%; Pred. No. 2.1e+02;
Matches 20; Conservative 23; Mismatches 28; Indels 8; Gaps 3;

QY 30 VSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRQLGQVPTQEFWDNLEKETEGLRQEMSKD 89
Db 23 LTQVEASLSPEDL-IKVLRQKKTLLSCIEKVVDHQI----KKFRDSF---SLALPQEVQEE 74

QY 90 LEEVKAKVQPYLDDFQKKW 108
Db 75 LEEIRSVIQRILETDKKNY 93

RESULT 13
D95153
hypothetical protein SPI323 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95153
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: D95153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KUR>
A;Cross-references: UNIPROT:Q97QA2; GB:AE005672; PIDN:AAK75421.1; PID:g14972804; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SPI323

Query Match 10.5%; Score 60.5; DB 2; Length 107;
Best Local Similarity 23.5%; Pred. No. 2.2e+02;
Matches 23; Conservative 17; Mismatches 35; Indels 23; Gaps 2;

QY 6 SPWDRVKDLATVYVDVLKDSGRDY-----VSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60
Db 4 SVFSTMQDIENVATDIIKSYDNEIYTYKAVSQEELEKLEKSYSDEKSHEELVSIES----- 58

QY 61 RQLGQVPTQEFWDNLEKETEGLRQEMSKOLEEVKAKVQ 98
Db 59 -----NLEMKQQLIDEVNKTIKENDANIQ 83

RESULT 14
D82445
hypothetical protein VCA0551 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82445
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82445
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-76 <HEI>
A;Cross-references: UNIPROT:Q9KM38; GB:AE004386; GB:AE003853; NID:g9657957; PIDN:AAF964;
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C;Genetics:
A;Gene: VCA0551
A;Map position: 2

Query Match 10.3%; Score 59.5; DB 2; Length 76;
Best Local Similarity 22.0%; Pred. No. 1.8e+02;
Matches 11; Conservative 11; Mismatches 13; Indels 15; Gaps 1;

QY 69 QEFWDNLEKETEGLRQE-----MSKDL EEVKAKVQPYLDD 103
Db 12 RRYWMNIRDRIEAEIQEIYVACSEGLATVNLLEQQLEQLRGKAPWSDE 61

RESULT 15
JU0038
nonhistone chromosomal protein HMG - Tetrahymena pyriformis
C;Species: Tetrahymena pyriformis
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-2004
C;Accession: JU0038
R;Hayashi, T.; Hayashi, H.; Iwai, K.
J. Biochem. 105, 577-581, 1989
A;Title: Tetrahymena HMG nonhistone chromosomal protein. Isolation and amino acid sequen
A;Reference number: JU0038; MUID:89340384; PMID:2760016
A;Accession: JU0038
A;Molecule type: protein
A;Residues: 1-99 <HAY>
A;Cross-references: UNIPROT:P40625
A;Note: this HMG is similar to the central part of vertebrate HMG1
A;Note: Ser-16 and Thr-42 and/or Ser-43 are 6-7% phosphorylated
C;Genetics:
A;Genetic code: SGC5
C;Superfamily: HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus; phosphoprotein
F;8-83/Domain: HMG box homology <HMG1>
F;16,43/Binding site: phosphate (Ser) (covalent) (partial) #status experimental
F;42/Binding site: phosphate (Thr) (covalent) (partial) #status experimental

Query Match 10.3%; Score 59.5; DB 2; Length 99;
Best Local Similarity 21.7%; Pred. No. 2.5e+02;
Matches 23; Conservative 18; Mismatches 32; Indels 33; Gaps 4;

QY 3 PPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRE 62
Db 10 PPKRP-----LSAFF--LFKQHNYDQVKKENPNAKITELTSIAEKKWKHVT----- 53

QY 63 QLGPVTQEFWDNLEKETEGLRQEMSKDL EEVKAKVQPYLDDFQKKW 108
Db 54 -----EKEKKKYEGLQQ-----EAKAKYEKDMQAYEKY 82

Search completed: December 21, 2004, 12:34:46
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 12:19:19 ; Search time 39 Seconds
(without alignments)
185.350 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_133
Perfect score: 576
Sequence: 1 DEPPQSPWDRVKDLATVYVD.....LEEVKAKVQPYLDDFQKKWQ 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 317198

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 143 | 24.8 | 44 | 2 | US-08-292-870-2 |
| 2 | 133 | 23.1 | 64 | 2 | US-08-292-870-1 |
| 3 | 114 | 19.8 | 25 | 2 | US-08-292-870-4 |
| 4 | 83 | 14.4 | 32 | 2 | US-08-292-870-3 |
| 5 | 81 | 14.1 | 16 | 1 | US-07-959-946-5 |
| 6 | 81 | 14.1 | 16 | 1 | US-08-333-577-5 |
| 7 | 81 | 14.1 | 16 | 5 | PCT-US92-08634-5 |
| 8 | 67.5 | 11.7 | 87 | 1 | US-08-685-764-4 |
| 9 | 67 | 11.6 | 105 | 4 | US-09-513-999C-6681 |
| 10 | 66.5 | 11.5 | 105 | 1 | US-08-241-853-11 |
| 11 | 66.5 | 11.5 | 105 | 2 | US-08-850-917-11 |
| 12 | 65.5 | 11.4 | 99 | 4 | US-09-147-875A-16 |
| 13 | 63.5 | 11.0 | 50 | 3 | US-09-695-458-9 |
| 14 | 63 | 10.9 | 103 | 4 | US-09-270-767-57235 |
| 15 | 63 | 10.9 | 106 | 4 | US-09-621-976-4439 |
| 16 | 62 | 10.8 | 65 | 2 | US-08-867-087B-34 |
| 17 | 61.5 | 10.7 | 98 | 2 | US-08-479-078-7 |
| 18 | 61.5 | 10.7 | 99 | 2 | US-08-710-749-10 |
| 19 | 61.5 | 10.7 | 99 | 4 | US-09-147-875A-11 |
| 20 | 61 | 10.6 | 66 | 2 | US-08-867-087B-70 |
| 21 | 61 | 10.6 | 100 | 4 | US-09-147-875A-12 |
| 22 | 60.5 | 10.5 | 37 | 3 | US-09-695-458-15 |
| 23 | 60 | 10.4 | 80 | 3 | US-09-183-861-61 |
| 24 | 60 | 10.4 | 80 | 3 | US-09-022-765-61 |
| 25 | 60 | 10.4 | 80 | 4 | US-09-551-974A-61 |
| 26 | 60 | 10.4 | 80 | 4 | US-09-565-501A-61 |
| 27 | 60 | 10.4 | 80 | 4 | US-09-639-206A-61 |

| | | | | | | |
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| 28 | 60 | 10.4 | 80 | 4 | US-09-874-923-61 | Sequence 61, Appl |
| 29 | 59.5 | 10.3 | 99 | 2 | US-08-710-749-12 | Sequence 12, Appl |
| 30 | 59.5 | 10.3 | 99 | 4 | US-09-147-875A-13 | Sequence 13, Appl |
| 31 | 58.5 | 10.2 | 96 | 2 | US-08-710-749-28 | Sequence 28, Appl |
| 32 | 58.5 | 10.2 | 96 | 4 | US-09-147-875A-28 | Sequence 28, Appl |
| 33 | 58.5 | 10.2 | 99 | 2 | US-08-710-749-15 | Sequence 15, Appl |
| 34 | 58 | 10.1 | 65 | 2 | US-08-867-087B-33 | Sequence 33, Appl |
| 35 | 58 | 10.1 | 103 | 4 | US-09-614-912-158 | Sequence 158, App |
| 36 | 58 | 10.1 | 103 | 4 | US-09-248-796A-26113 | Sequence 26113, A |
| 37 | 57.5 | 10.0 | 30 | 1 | US-08-182-175A-8 | Sequence 8, Appli |
| 38 | 57.5 | 10.0 | 30 | 5 | PCT-US92-06412-8 | Sequence 8, Appli |
| 39 | 57.5 | 10.0 | 94 | 1 | US-08-025-038-41 | Sequence 41, Appl |
| 40 | 57.5 | 10.0 | 99 | 2 | US-08-710-749-17 | Sequence 17, Appl |
| 41 | 57 | 9.9 | 13 | 5 | PCT-US94-01234-47 | Sequence 47, Appl |
| 42 | 57 | 9.9 | 99 | 4 | US-09-134-000C-6615 | Sequence 6615, Ap |
| 43 | 56.5 | 9.8 | 99 | 2 | US-08-710-749-11 | Sequence 11, Appl |
| 44 | 56.5 | 9.8 | 100 | 4 | US-09-147-875A-3 | Sequence 3, Appli |
| 45 | 56.5 | 9.8 | 108 | 2 | US-08-710-749-25 | Sequence 25, Appl |

ALIGNMENTS

RESULT 1
US-08-292-870-2
; Sequence 2, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-2

Query Match 24.8%; Score 143; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RQEMSKDLEEVKAKVQPYLDDFQKKWQ 109
Db 1 RQEMSKDLEEVKAKVQPYLDDFQKKWQ 27

RESULT 2
US-08-292-870-1
; Sequence 1, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-1

Query Match 23.1%; Score 133; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 EMSKDLEEVKAKVQPYLDDFQKKWQ 109
Db 1 EMSKDLEEVKAKVQPYLDDFQKKWQ 25

RESULT 3
US-08-292-870-4
; Sequence 4, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-4

Query Match 19.8%; Score 114; DB 2; Length 25;
Best Local Similarity 95.7%; Pred. No. 3.5e-05;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 SKDLEEVKAKVQPYLDDFQKKWQ 109
Db 1 SKDLEEVKAKVQPYLDDFQKKWQ 23

RESULT 4
US-08-292-870-3
; Sequence 3, Application US/08292870
; Patent No. 5814467

; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 581467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa can be either E (Glu)
; OTHER INFORMATION: or F (Phe)"
US-08-292-870-3
Query Match 14.4%; Score 83; DB 2; Length 32;
Best Local Similarity 93.8%; Pred. No. 0.071;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 94 KAKVQPYLDDFQKKWQ 109
Db 1 KAKVQPYLDDXQKKWQ 16
RESULT 5
US-07-959-946-5
; Sequence 5, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.

; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-946-5
Query Match 14.1%; Score 81; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 96 KVQPYLDDFQKKWQ 109
Db 1 KVQPYLDDFQKKWQ 14
RESULT 6
US-08-333-577-5
; Sequence 5, Application US/08333577
; Patent No. 5786206
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-577-5

Query Match 14.1%; Score 81; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KVQPYLDDFQKKWQ 109
Db 1 KVQPYLDDFQKKWQ 14

RESULT 7
PCT-US92-08634-5
Sequence 5, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-5
Query Match 14.1%; Score 81; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 KVQPYLDDFQKKWQ 109
Db 1 KVQPYLDDFQKKWQ 14
RESULT 8
US-08-685-764-4
Sequence 4, Application US/08685764
Patent No. 5800982
GENERAL INFORMATION:
APPLICANT: HASEGAWA, AKIRA
APPLICANT: MAKI, NOBORU
APPLICANT: YAGI, SHINTARO
APPLICANT: KASHIWAKUMA, TOMIKO
TITLE OF INVENTION: ANTIGENIC PEPTIDES FOR GROUPING
TITLE OF INVENTION: HEPATITIS C VIRUS, KIT COMPRISING THE SAME AND
TITLE OF INVENTION: METHODS FOR ITS GROUPING USING THE SAME
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,764
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/092,192
FILING DATE: 15-JUL-1993
APPLICATION NUMBER: JP 212061/92
FILING DATE: 16-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 316634/92
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 316635/92
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104754/93
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, LINDA M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 42822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-764-4

Query Match 11.7%; Score 67.5; DB 1; Length 87;
Best Local Similarity 24.2%; Pred. No. 9.7;
Matches 23; Conservative 22; Mismatches 39; Indels 11; Gaps 3;

QY 13 DLATVYVDVKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPTQEFW 72
Db 1 EFATGCVSII---GRLHINQRAVVPDKVEVYEAFADEMEECASRAALIEE-----GQRIA 52

QY 73 DNLEKETEGLRQBSMKDLEEVKAKVQ---PYLDDF 104
Db 53 EMLKSKIQGLLQASKQAQDIKPAVQTSWPKVEQF 87

RESULT 9
US-09-513-999C-6681
; Sequence 6681, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6681
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6681

Query Match 11.6%; Score 67; DB 4; Length 105;
Best Local Similarity 28.4%; Pred. No. 14;
Matches 19; Conservative 16; Mismatches 28; Indels 4; Gaps 2;

QY 39 GKQLNLKLLD-NWDSVTSTFSKLREQLGPTQEFWDNLEKETEG---LRQEMSKDLEEVK 94
Db 7 GKEQQLDIMNKYQQLSRLDEILSRIAKETEEIKDLEEQLTEGQIAANEALKKDLEGVI 66

QY 95 AKVQPYL 101
Db 67 SGLQEYL 73

RESULT 10
US-08-241-853-11
; Sequence 11, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853

; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-241-853-11

Query Match 11.5%; Score 66.5; DB 1; Length 105;
Best Local Similarity 27.7%; Pred. No. 15;
Matches 26; Conservative 11; Mismatches 28; Indels 29; Gaps 4;

QY 8 WDRVKDLATVYVDVLKD-----SGRDYVSQFEGS--ALGK 40
Db 12 WDQLKDLAAFCCKNLQDAENFFQFGDADDLKAWLQDAHRLLSGED-VGQDEGATRALGK 70

QY 41 QLNKLLDNWDSVTSTFSKLREQLGPTQEFWDN 74
Db 71 K-HKDFLEELESRGVMKLEQQAQGFPEEFRDS 103

RESULT 11
US-08-850-917-11
; Sequence 11, Application US/08850917
; Patent No. 5854045
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,917
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,853
; FILING DATE: 12-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:


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; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-850-917-11

Query Match      11.5%; Score 66.5; DB 2; Length 105;
Best Local Similarity 27.7%; Pred. No. 15;
Matches 26; Conservative 11; Mismatches 28; Indels 29; Gaps 4;

QY      8 WDRVKDLATVYVDVLKD-----SGRDYVSQFEGS--ALGK 40
Db      12 WDQLKDLAAFCCKQLQDAENFFQFGDADDLKAWLQDAHRLLSGED-VQDEGATRALGK 70

QY      41 QLNKLKLDNWDVSTSFSKLREQLGPVTQEFWDN 74
Db      71 K-HKDFLEELESRGVMEKLEQQAAQGFPPEFRDS 103

RESULT 12
US-09-147-875A-16
; Sequence 16, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-16

Query Match      11.4%; Score 65.5; DB 4; Length 99;
Best Local Similarity 24.2%; Pred. No. 18;
Matches 24; Conservative 19; Mismatches 37; Indels 19; Gaps 3;

QY      20 DVLKDSGRDYVSQFEGSALGKQLNLK-----LLDNWDSVTSTFSKLRQL----- 64
Db      3 EIDESDSEDYLKEGERAPLQSKLDTKKAKUSKLEELSDKIDELDAEIAKLEVLQKDAEGN 62

QY      65 GPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVPYLDD 103
Db      63 NNVEAYFKEGLEKTT----AEKKAEELEKAEADLKKAVDE 97

RESULT 13
US-09-695-458-9
; Sequence 9, Application US/09695458
; Patent No. 6380361
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: Educational Kit and Method Containing No. 6380361el Alpha Helical
; TITLE OF INVENTION: Protein-34
; FILE REFERENCE: 99-78
; CURRENT APPLICATION NUMBER: US/09/695,458
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/162,623
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Mus musculus
```

```

US-09-695-458-9

Query Match      11.0%; Score 63.5; DB 3; Length 50;
Best Local Similarity 51.9%; Pred. No. 12;
Matches 14; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY      59 KLRQLGPVTQEFWDNLEKETEGLRQE 85
Db      11 KASEELGE-AQTVWDNLQKELDLLREE 36

RESULT 14
US-09-270-767-57235
; Sequence 57235, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57235
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57235

Query Match      10.9%; Score 63; DB 4; Length 103;
Best Local Similarity 28.6%; Pred. No. 34;
Matches 18; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

QY      7 PWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLDNWDVSTSTFSKLR-EQLG 65
Db      20 PFEKLADLAREDLEAHALKGTXYIEDLKG-AVKKDLGYELLKPYDGTRELIIKKIKDEDPG 78

QY      66 PVT 68
Db      79 KVT 81

RESULT 15
US-09-621-976-4439
; Sequence 4439, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4439
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4439

Query Match      10.9%; Score 63; DB 4; Length 106;
Best Local Similarity 23.9%; Pred. No. 36;
Matches 21; Conservative 24; Mismatches 33; Indels 10; Gaps 3;

QY      12 KDLATVYVDVLKDSGR-DYVSQFEGSALGKQLNLKLDNWDVSTSTFSKLRQLGPVTQE 70
Db      11 RNIIISLNMMDLERTQRIDEANQ-----KLLKIQEREDKIQRLESEIIQTRGLVEDE 62

QY      71 FWDNLEKETEGLRQEMSKDLEEVKAKVQ 98
Db      63 EWEX-ENRRTMERERALQEEETARLE 89
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Search completed: December 21, 2004, 12:33:58
Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 12:05:04 ; Search time 38 Seconds
(without alignments)
98.749 Million cell updates/sec

Title: US-09-803-918A-2_COPY_75_113
Perfect score: 201
Sequence: 1 DSVTSTFSLRQLGPVTQEFWDNLEKETEGLRQEMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 9448

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Minimum DB seq length: 0
Maximum DB seq length: 41
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : PIR 79:*
1:  pir1:
2:  pir2:
3:  pir3:
4:  pir4:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1 | 40 | 19.9 | 33 | 2 | S52151 | hypothetical prote |
| 2 | 37 | 18.4 | 40 | 2 | H81592 | hypothetical prote |
| 3 | 36 | 17.9 | 34 | 2 | G84147 | hypothetical prote |
| 4 | 36 | 17.9 | 35 | 2 | AH1838 | cytochrome c6 [imp |
| 5 | 34 | 16.9 | 19 | 2 | E60977 | 14-3-3 protein hom |
| 6 | 34 | 16.9 | 30 | 2 | S74192 | crotoxin inhibitor |
| 7 | 34 | 16.9 | 40 | 2 | T07516 | hypothetical prote |
| 8 | 33 | 16.4 | 39 | 2 | G82613 | hypothetical prote |
| 9 | 32.5 | 16.2 | 27 | 2 | PQ0844 | DNA-binding protei |
| 10 | 32 | 15.9 | 31 | 2 | PS0350 | myohemerythrin iso |
| 11 | 32 | 15.9 | 34 | 2 | C56635 | tubulin alpha chai |
| 12 | 32 | 15.9 | 35 | 2 | A54257 | deoxynucleoside ki |
| 13 | 32 | 15.9 | 35 | 2 | B82012 | hypothetical prote |
| 14 | 32 | 15.9 | 39 | 2 | S70798 | Ivi protein I - Vi |
| 15 | 32 | 15.9 | 40 | 2 | C95169 | hypothetical prote |
| 16 | 31 | 15.4 | 31 | 2 | E82856 | hypothetical prote |
| 17 | 31 | 15.4 | 33 | 2 | B56635 | tubulin alpha chai |
| 18 | 31 | 15.4 | 37 | 2 | S26954 | peptide YY-related |
| 19 | 31 | 15.4 | 40 | 2 | A59005 | thymosin beta - se |
| 20 | 30.5 | 15.2 | 29 | 2 | S17432 | H+-transporting tw |
| 21 | 30 | 14.9 | 15 | 2 | PA0091 | methionine adenosy |
| 22 | 30 | 14.9 | 27 | 1 | SECH | secretin - chicken |
| 23 | 30 | 14.9 | 29 | 2 | C61384 | trachael mucin gly |
| 24 | 30 | 14.9 | 30 | 2 | H72312 | hypothetical prote |
| 25 | 30 | 14.9 | 35 | 2 | D81622 | hypothetical prote |
| 26 | 30 | 14.9 | 35 | 2 | S53728 | fructosyllysine-sp |
| 27 | 30 | 14.9 | 36 | 2 | PT0430 | leucyl aminopeptid |
| 28 | 30 | 14.9 | 36 | 2 | A60343 | transforming prote |
| 29 | 30 | 14.9 | 36 | 2 | C64039 | hypothetical prote |

ALIGNMENTS

```

RESULT 1
S52151
hypothetical protein - phase 2C (fragment)
C:Species: phase 2C
A:Note: host Bacillus subtilis
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:Accession: S52151
R:Hoet, P.
submitted to the EMBL Data Library, December 1993
A:Description: Isolation and characterization of Bacillus subtilis phase 2C
A:Reference number: S52151
A:Accession: S52151
A:Molecule type: DNA
A:Residues: 1-33 <HOE>
A:Cross-references: EMBL:X75889
C:Genetics:
A:Start codon: GTG

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Query Match 19.9%; Score 40; DB 2; Length 33;
Best Local Similarity 47.6%; Pred. No. 1.7e+02;
Matches 10; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

Qy 15 G P V T Q E F W D N L E --- K E T E G 31
 D b 6 G A V T N E E F K D R L Q V F N K E V Q G 26

RESULT 2
H81592
Hypothetical protein CP0296 [imported] - Chlamydoiphila pneumoniae (strain AR39)
C:Species: Chlamydoiphila pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81592
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: H81592
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-40 <REA>
A:Cross-references: UNIPROT:Q9K2A3; GB:AE002191; GB:AE002161; NID:g7189216; PIDN:AAF38
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0296

```
Query Match      18.4%; Score 37; DB 2; Length 40;
Best Local Similarity 30.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
```

QY 1 DSVTSTFSLREQLGPVTQE 20

G82613
hypothetical protein XF1988 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: G82613
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: G82613
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-39 <SIM>
A/Cross-references: UNIPROT:Q9PBZ7; GB:AE004018; GB:AE003849; NID:g9107093; PIDN:AAF8479
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics: A:Gene: XF1988

```
Query Match      16.4%; Score 33; DB 2; Length 39;
Best Local Similarity 38.9%; Pred. No. 1.5e+03;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
```

| | | | |
|----|----|---------------------|----|
| Qy | 12 | EQLGPVTQEFWDNLEKET | 29 |
| | | : : : | |
| Db | 12 | EQVKA VNDFYWISLSKVT | 29 |

RESULT 9
PQ0844
DNA-binding protein AcBBP1 - Azorhizobium caulinodans (fragment)
C;Species: Azorhizobium caulinodans
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0844
R;Welters, P.; Metz, B.; Felix, G.; Palme, K.; Szczyglowski, K.; de Bruijn, F.J.
Plant Physiol. 102, 1095-1107, 1993
A;Title: Interaction of a rhizobial DNA-binding protein with the promoter region of a pl
A;Reference number: PQ0844; MUID:94105338; PMID:8278541
A;Accession: PQ0844
A;Molecule type: protein
A;Residues: 1-27 <WEL>
A;Cross-references: UNIPROT:Q7M1A8
A;Experimental source: strain ORS571

```

Query Match          16.2%;      Score 32.5;   DB 2;   Length 27;
Best Local Similarity 44.4%;      Pred. No. 1.1e+03;
Matches 8; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

```

| | | | |
|----|---|-------------------|----|
| Qy | 3 | VTSTFSKLRQLGPVTQE | 20 |
| | | | |
| Db | 7 | VGRNFARLRQEKGLTQE | 23 |

RESULT 10
PS0350
myohemerythrin isoform II - sipunculid (Phascolopsis gouldii) (fragment)
C;Species: Phascolopsis gouldii
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: PS0350

R; Long, R.C.; Zhang, J.H.; Kurtz Jr., D.M.; Negri, A.; Tedeschi, G.; Bonomi, F.
submitted to JIPID, April 1992
A; Reference number: JS0678
A; Accession: PS0350
A; Molecule type: protein
A; Residues: 1-31 <LON>
A; Cross-references: UNIPROT:P27687
C; Comment: This myohemerythrin is a monomeric oxygen-binding protein found in t
C; Superfamily: hemerythrin
C; Keywords: oxygen carrier

Query Match 15.9%; Score 32; DB 2; Length 31;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

| | |
|----------------|----------------------|
| Qy | 21 FWDNLEKETEGLRQ 34 |
| | : : : |
| D _b | 17 FYDLLDDEHKGLFQ 30 |

RESULT 11

C56635

tubulin alpha chain, brain-specific isotype (clone pTUB6) - chum salmon (fragment)

C;Species: Oncorhynchus keta (chum salmon)

C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 10-Jul-1998

C;Accession: C56635

R;Coe, I.R.; Munro, R.; Sherwood, N.M.

DNA Seq. 3, 257-262, 1992

A;Title: Isolation of different brain-specific isotypes of alpha-tubulins from

A;Reference number: A56635; MUID:93208376; PMID:1296820

A;Contents: brain

A;Accession: C56635

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-34 <COE>

A;Note: sequence extracted from NCBI backbone (NCBIN:128392, NCBIP:128391)

C;Superfamily: tubulin

F;28/Binding site: polyglutamate (Glu) (covalent) #status predicted

F;33-34/Cleavage site: Glu-Tyr (tubulin-specific carboxypeptidase) #status predicted

F;33-34/Cross-link: peptide (Glu-Tyr) (by tubulin-tyrosine ligase) #status predicted

Query Match 15.9%; Score 32; DB 2; Length 34;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 8; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

| | | | | | |
|----|---|---------------------|-----|-----------|----|
| Qy | 7 | FSKLREQLPVTQEF | --- | WDNLEKETE | 30 |
| | | | : | : | |
| | | : | : | : | : |
| | | : | : | : | : |
| Db | 1 | FSEAREDMAALEKDVEEVG | VD | SIEGE | 28 |
| | | : | : | : | : |
| | | : | : | : | : |
| | | : | : | : | : |

RESULT 12
A54257
deoxynucleoside kinase complex I S-component - Lactobacillus acidophilus (fragment)
C;Species: Lactobacillus acidophilus
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54257
R;Ikeda, S.; Ma, G.T.; Ives, D.H.
Biochemistry 33, 5328-5334, 1994
A;Title: Heterodimeric deoxynucleoside kinases of Lactobacillus acidophilus R-2
A;Reference number: A54257; MUID:94227067; PMID:8172906

Query Match 15.9%; Score 32; DB 2; Length 35;
Best Local Similarity 39.1%; Pred. No. 1.7e+03;
Matches 9; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 12:02:34 ; Search time 189 Seconds
(without alignments)
118.728 Million cell updates/sec

Title: US-09-803-918A-2_COPY_75_113
Perfect score: 201
Sequence: 1 DSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 56135

Minimum DB seq length: 0
Maximum DB seq length: 41

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|----------------------|
| 1 | 51.5 | 25.6 | 37 | 2 | Q6KGF3 bacterioph |
| 2 | 45.5 | 22.6 | 39 | 2 | Q8WTG3 pepsis sp. |
| 3 | 45.5 | 22.6 | 39 | 2 | Q8WT10 cephus sp. |
| 4 | 45 | 22.4 | 32 | 2 | Q73DP3 bacillus ce |
| 5 | 45 | 22.4 | 32 | 2 | AAS39602 bacillus |
| 6 | 43 | 21.4 | 41 | 2 | Q13587 homo sapien |
| 7 | 41 | 20.4 | 32 | 2 | Q53103 rhodobacter |
| 8 | 40 | 19.9 | 40 | 2 | Q62886 canis famil |
| 9 | 39.5 | 19.7 | 29 | 2 | P97599 rattus norv |
| 10 | 39.5 | 19.7 | 36 | 2 | O45208 acanthokara |
| 11 | 39 | 19.4 | 27 | 2 | Q9MHZ4 drosophila |
| 12 | 39 | 19.4 | 27 | 2 | Q9MHZ6 drosophila |
| 13 | 39 | 19.4 | 27 | 2 | Q9MHZ8 drosophila |
| 14 | 39 | 19.4 | 27 | 2 | Q9MI20 drosophila |
| 15 | 39 | 19.4 | 27 | 2 | Q9MI26 drosophila |
| 16 | 39 | 19.4 | 27 | 2 | Q9MI28 drosophila |
| 17 | 39 | 19.4 | 27 | 2 | Q9MI30 drosophila |
| 18 | 39 | 19.4 | 34 | 2 | Q8LVV4 ceratitidis r |
| 19 | 39 | 19.4 | 34 | 2 | Q8LVV5 bactrocera |
| 20 | 39 | 19.4 | 34 | 2 | Q8LVV6 bactrocera |
| 21 | 39 | 19.4 | 34 | 2 | Q8LYC8 ceratitidis r |
| 22 | 39 | 19.4 | 34 | 2 | Q8LYD4 bactrocera |
| 23 | 39 | 19.4 | 34 | 2 | Q8LYD8 bactrocera |
| 24 | 39 | 19.4 | 34 | 2 | Q8LYD9 bactrocera |
| 25 | 39 | 19.4 | 34 | 2 | Q8LYE0 bactrocera |
| 26 | 39 | 19.4 | 34 | 2 | Q8LYE2 bactrocera |
| 27 | 39 | 19.4 | 34 | 2 | Q8LYE4 bactrocera |
| 28 | 39 | 19.4 | 34 | 2 | Q8LYE6 anastrepha |
| 29 | 39 | 19.4 | 34 | 2 | Q8LYE8 anastrepha |
| 30 | 38 | 18.9 | 26 | 2 | Q7R9A2 plasmodium |
| 31 | 38 | 18.9 | 27 | 2 | Q9MI00 drosophila |

| | | | | | | |
|----|----|------|----|---|--------|----------------------|
| 32 | 38 | 18.9 | 27 | 2 | Q9MI02 | Q9mi02 drosophila |
| 33 | 38 | 18.9 | 27 | 2 | Q9MI04 | Q9mi04 drosophila |
| 34 | 38 | 18.9 | 27 | 2 | Q9MI06 | Q9mi06 bactrocera |
| 35 | 38 | 18.9 | 27 | 2 | Q9MI14 | Q9mi14 drosophila |
| 36 | 38 | 18.9 | 27 | 2 | Q9MI22 | Q9mi22 drosophila |
| 37 | 38 | 18.9 | 27 | 2 | Q9MI24 | Q9mi24 drosophila |
| 38 | 38 | 18.9 | 30 | 2 | Q9K532 | Q9k532 listeria mo |
| 39 | 38 | 18.9 | 34 | 2 | Q8LVV3 | Q8lvv3 ceratitidis c |
| 40 | 38 | 18.9 | 34 | 2 | Q8LYB7 | Q8lyb7 toxotrypana |
| 41 | 38 | 18.9 | 34 | 2 | Q8LYB9 | Q8lyb9 rhagoletis |
| 42 | 38 | 18.9 | 34 | 2 | Q8LYC5 | Q8lyc5 dacus demme |
| 43 | 38 | 18.9 | 34 | 2 | Q8LYC7 | Q8lyc7 dacus cilia |
| 44 | 38 | 18.9 | 34 | 2 | Q8LYD2 | Q8lyd2 ceratitidis c |
| 45 | 38 | 18.9 | 34 | 2 | Q8LYD6 | Q8lyd6 bactrocera |

ALIGNMENTS

RESULT 1
Q6KGF3
ID Q6KGF3 PRELIMINARY; PRT; 37 AA.
AC Q6KGF3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Bacteriophage Felix 01.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
OX NCBI_TaxID=77775;
RN [1]
RP SEQUENCE FROM N.A.
RA Sriranganathan N., Whichard J.M., Pierson F.W., Kapur V., Weigt L.A.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF320576; AAQ14805.1; -.
KW Hypothetical protein.
SQ SEQUENCE 37 AA; 4308 MW; 551EF5EA0BAA0CAD CRC64;

Query Match 25.6%; Score 51.5; DB 2; Length 37;
Best Local Similarity 38.2%; Pred. No. 54;
Matches 13; Conservative 3; Mismatches 13; Indels 5; Gaps 1;

Qy 3 VTSTFSKLRQLG-----PVTQEFWDNLEKETEG 31
Db 2 IEKVFFKLARYLAGKTDTPIDDFVDNLEKAFKG 35
RESULT 2
Q8WTG3
ID Q8WTG3 PRELIMINARY; PRT; 39 AA.
AC Q8WTG3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Engrailed (Fragment).
OS Pepsis sp. MFW-2001.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Pompilidae; Pepsis.
OX NCBI_TaxID=173816;
RN [1]
RP SEQUENCE FROM N.A.
RA Whiting M.F.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF275780; AAL35008.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.

DR PROSITE; PS50071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4687 MW; 42A28CCE81441488 CRC64;

Query Match 22.6%; Score 45.5; DB 2; Length 39;
Best Local Similarity 42.9%; Pred. No. 3e+02;
Matches 12; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 12 EQLGPVTQEFWDNLEKETEGLRQEMSKD 39
||| : ||| : || || ||| : ||
Db 3 EQLARLKREFAEN-RYLTERRRRQQLSRD 29
||| : ||| : || || ||| : ||

RESULT 3
Q8WTIO PRELIMINARY; PRT; 39 AA.
AC Q8WTIO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Engrailed (Fragment).
OS Cephus sp. MFW-2001.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Cephoidea; Cephidae; Cephus.
OX NCBI_TaxID=173785;
RN [1]
RP SEQUENCE FROM N.A.
RA Whiting M.F.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF275760; AAL34991.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4687 MW; 42A28CCE81441488 CRC64;

Query Match 22.6%; Score 45.5; DB 2; Length 39;
Best Local Similarity 42.9%; Pred. No. 3e+02;
Matches 12; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 12 EQLGPVTQEFWDNLEKETEGLRQEMSKD 39
||| : ||| : || || ||| : ||
Db 3 EQLARLKREFAEN-RYLTERRRRQQLSRD 29
||| : ||| : || || ||| : ||

RESULT 4
Q73DP3 PRELIMINARY; PRT; 32 AA.
AC Q73DP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE0669;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;

RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017266; AAS39602.1; -.
DR TIGR; BCE0669; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 32 AA; 3619 MW; C9161226273EE94C CRC64;

Query Match 22.4%; Score 45; DB 2; Length 32;
Best Local Similarity 39.3%; Pred. No. 2.8e+02;
Matches 11; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLRQLGPVTQEFWDNLEKE 28
: || || || || : || || || || : ||
Db 2 NGVLSTFTLCKFALAYTMEIWCNAKDD 29
: || || || || : || || || || : ||

RESULT 5
AAS39602 PRELIMINARY; PRT; 32 AA.
ID AAS39602
AC AAS39602;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN BCE0669.
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017266; AAS39602.1; -.
DR TIGR; BCE0669; -.
KW Hypothetical protein.
SQ SEQUENCE 32 AA; 3619 MW; C9161226273EE94C CRC64;

Query Match 22.4%; Score 45; DB 2; Length 32;
Best Local Similarity 39.3%; Pred. No. 2.8e+02;
Matches 11; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLRQLGPVTQEFWDNLEKE 28
: || || || || : || || || || : ||
Db 2 NGVLSTFTLCKFALAYTMEIWCNAKDD 29
: || || || || : || || || || : ||

RESULT 6
Q13587 PRELIMINARY; PRT; 41 AA.
ID Q13587
AC Q13587;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fatty acid synthase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96278786; PubMed=8662758;
RA Hsu M.H., Chirala S.S., Wakil S.J.;
RT "Human fatty-acid synthase gene. Evidence for the presence of two
RT promoters and their functional interaction.";
RL J. Biol. Chem. 271:13584-13592(1996).
DR EMBL; U52428; AAC50536.1; -.;

DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; NucIear protein.
FT NON_TER 1 1
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 4478 MW; E803EA629E459B67 CRC64;

Query Match 19.7%; Score 39.5; DB 2; Length 36;
Best Local Similarity 39.3%; Pred. No. 1.5e+03;
Matches 11; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 12 EQLGPVTQEFWDNLEKETEGLRQEMSKD 39
||| : :|| :| || ||| :|| :|
Db 3 EQLQLKKKFFQEN-RYLTEKRRQDLAND 29

RESULT 11
Q9MHZ4
ID Q9MHZ4 PRELIMINARY; PRT; 27 AA.
AC Q9MHZ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN Name=mt:Cyt-b; Synonyms=cytb;
OS Drosophila elegans (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=30023;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12927135;
RA Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
RT "Macroevolutionary relationships of species of Drosophila melanogaster
RT group based on mtDNA sequences.";
RL Mol. Phylogenet. Evol. 28:518-528(2003).
DR EMBL; AF164596; AAF81402.1; -.
DR FlyBase; FBgn0042070; Dele\mt:Cyt-b.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 27 AA; 3300 MW; D772900B152680C8 CRC64;

Query Match 19.4%; Score 39; DB 2; Length 27;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 14 LGPVTQEFWDNL 25
: |: :|||
Db 14 INPLVSKWWDNL 25

RESULT 12
Q9MHZ6
ID Q9MHZ6 PRELIMINARY; PRT; 27 AA.
AC Q9MHZ6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN Name=mt:Cyt-b; Synonyms=cytb;
OS Drosophila eugracilis (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=29029;
RN [1]
RP SEQUENCE FROM N.A.

RX PubMed=12927135;
RA Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
RT "Macroevolutionary relationships of species of Drosophila melanogaster
RT group based on mtDNA sequences.";
RL Mol. Phylogenet. Evol. 28:518-528(2003).
DR EMBL; AF164595; AAF81400.1; -.
DR FlyBase; FBgn0042058; Deug\mt:Cyt-b.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 27 AA; 3300 MW; D772900B035C3C18 CRC64;

Query Match 19.4%; Score 39; DB 2; Length 27;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 14 LGPVTQEFWDNL 25
: |: :|||
Db 14 INPLVSKWWDNL 25

RESULT 13
Q9MHZ8
ID Q9MHZ8 PRELIMINARY; PRT; 27 AA.
AC Q9MHZ8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN Name=mt:Cyt-b; Synonyms=cytb;
OS Drosophila ficusphila (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=30025;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12927135;
RA Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
RT "Macroevolutionary relationships of species of Drosophila melanogaster
RT group based on mtDNA sequences.";
RL Mol. Phylogenet. Evol. 28:518-528(2003).
DR EMBL; AF164594; AAF81398.1; -.
DR FlyBase; FBgn0042053; Dfic\mt:Cyt-b.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 27 AA; 3300 MW; D772900B035C3C18 CRC64;

Query Match 19.4%; Score 39; DB 2; Length 27;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 14 LGPVTQEFWDNL 25
: |: :|||
Db 14 INPLVSKWWDNL 25

RESULT 14
Q9MI20
ID Q9MI20 PRELIMINARY; PRT; 27 AA.
AC Q9MI20;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN Name=mt:Cyt-b; Synonyms=cytb;
OS Drosophila kikkawai (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

```
OX  NCBI_TaxID=30033;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  PubMed=12927135;
RA  Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
RT  "Macroevolutionary relationships of species of Drosophila melanogaster
RL  group based on mtDNA sequences.";
RL  Mol. Phylogenet. Evol. 28:518-528(2003).
DR  EMBL; AF164583; AAF81376.1; -.
DR  FlyBase; FBgn0042046; Dkik\mt:Cyt-b.
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON TER 1
SQ  SEQUENCE 27 AA; 3313 MW;  CD5B900B1530EC18 CRC64;

Query Match      19.4%; Score 39; DB 2; Length 27;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 14 LGPVTQEFWDNL 25
Db 14 INPLVKNKWDNL 25

RESULT 15
Q9MI26
ID Q9MI26 PRELIMINARY; PRT; 27 AA.
AC Q9MI26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN Name=mt:Cyt-b; Synonyms=cytb;
OS Drosophila auraria (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=47315;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12927135;
RA Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
RT "Macroevolutionary relationships of species of Drosophila melanogaster
RL group based on mtDNA sequences.";
RL Mol. Phylogenet. Evol. 28:518-528(2003).
DR EMBL; AF164580; AAF81370.1; -.
DR FlyBase; FBgn0042077; Daur\mt:Cyt-b.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 27 AA; 3313 MW;  CD5B900B1530EC18 CRC64;

Query Match      19.4%; Score 39; DB 2; Length 27;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 14 LGPVTQEFWDNL 25
Db 14 INPLVKNKWDNL 25

Search completed: December 21, 2004, 12:18:24
Job time : 192 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 12:05:32 ; Search time 151 Seconds
(without alignments)
92.652 Million cell updates/sec

Title: US-09-803-918A-2_COPY_75_113
Perfect score: 201
Sequence: 1 DSVTSTFSKLRQLGPVTQEFWDNLEKTEGLRQEMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 856990

Minimum DB seq length: 0
Maximum DB seq length: 41

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result | | Query | | Description | |
|--------|-------|-------|--------|-------------|--------------------|
| No. | Score | Match | Length | ID | |
| 1 | 89 | 44.3 | 16 | 6 | ABP57175 Breast ca |
| 2 | 80 | 39.8 | 16 | 4 | AAG62607 Apolipop |
| 3 | 60.5 | 30.1 | 37 | 4 | AAE02141 Mouse alp |
| 4 | 60.5 | 30.1 | 37 | 5 | AAU99633 Mouse sec |
| 5 | 56 | 27.9 | 22 | 2 | AAU18752 Lecithin: |
| 6 | 56 | 27.9 | 22 | 2 | AAY19006 Lecithin: |
| 7 | 56 | 27.9 | 22 | 2 | AAY19260 Lecithin: |
| 8 | 56 | 27.9 | 22 | 2 | AAY18489 Lecithin: |
| 9 | 56 | 27.9 | 22 | 8 | ADG20969 Apolipop |
| 10 | 56 | 27.9 | 22 | 8 | ADJ32911 Apo lipop |
| 11 | 55 | 27.4 | 31 | 8 | ADP80870 Mouse apo |
| 12 | 52 | 25.9 | 18 | 7 | ADC29662 Antioxi |
| 13 | 52 | 25.9 | 18 | 7 | ADC29658 Antioxi |
| 14 | 52 | 25.9 | 18 | 7 | ADC29661 Antioxi |
| 15 | 52 | 25.9 | 18 | 7 | ADC29657 Antioxi |
| 16 | 52 | 25.9 | 18 | 7 | ADC29659 Antioxi |
| 17 | 52 | 25.9 | 18 | 7 | ADC29660 Antioxi |
| 18 | 52 | 25.9 | 30 | 7 | ADC29669 Antioxi |
| 19 | 52 | 25.9 | 30 | 7 | ADC29665 Antioxi |
| 20 | 52 | 25.9 | 30 | 7 | ADC29668 Antioxi |
| 21 | 52 | 25.9 | 30 | 7 | ADC29670 Antioxi |
| 22 | 52 | 25.9 | 30 | 7 | ADC29664 Antioxi |
| 23 | 52 | 25.9 | 30 | 7 | ADC29667 Antioxi |
| 24 | 52 | 25.9 | 30 | 7 | ADC29666 Antioxi |
| 25 | 51 | 25.4 | 22 | 2 | AAR48545 Sequence |

SUMMARIES

ALIGNMENTS

RESULT 1
ABP57175
ID ABP57175 standard; peptide; 16 AA.
XX

AC ABP57175;

XX 16-APR-2003 (first entry)

DE Breast cancer associated tryptic digest peptide SEQ ID NO:37.

XX KW Breast cancer associated feature; BP; BPI; breast cancer; diagnosis;
KW breast cancer associated protein isoform; cytostatic; gene therapy.

XX OS Homo sapiens.
OS Synthetic.

XX WO200288750-A2.

XX PD 07-NOV-2002.

XX PF 02-MAY-2002; 2002WO-GB002022.

XX PR 02-MAY-2001; 2001GB-00010790.

XX PR 27-JUL-2001; 2001GB-00018385.

XX PR 14-AUG-2001; 2001GB-00019791.

XX PR 16-AUG-2001; 2001GB-00020045.

XX PR 22-NOV-2001; 2001GB-00028062.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMC;

XX DR WPI; 2003-175048/17.

XX PT Screening, diagnosing or determining the stage or severity of breast

XX PT cancer, comprises analyzing and quantitatively detecting Breast Cancer-

XX PT Associated Features or Breast Cancer-Associated Protein Isoforms in a

XX PS biological sample.

XX PS Disclosure; Page 18; 88pp; English.

XX CC The present invention describes a method for screening, diagnosing or

XX CC determining the stage or severity of breast cancer, identifying a subject

XX CC at risk of developing breast cancer, or monitoring the effect of therapy

XX CC administered to a subject with breast cancer, by generating a two-

XX CC dimensional array of features comprising breast cancer-associated

XX CC features (BFs), or quantitatively detecting breast cancer-associated

XX CC protein isoforms (BPIs). Also described: (i) an antibody capable of

CC immunospecifically binding to one of the BPIs; (2) a pharmaceutical
CC compositions comprising: (a) a BPI, or a nucleic acid encoding a BPI, and
CC a carrier; or (b) the antibody of (1), or a fragment or derivative of the
CC antibody, and a carrier; (3) screening for agents that interact with one
CC or more BPIs, BPI fragments, polypeptides related to BPIs, or BPI-fusion
CC proteins; (4) screening for or identifying agents that modulate the
CC expression or activity of one or more BPIs, a BPI fragment, a BPI-related
CC polypeptide, or BPI-fusion proteins; and (5) treating or preventing
CC breast cancer. BPIs have cytostatic activity and can be used in gene
CC therapy. Methods and kits comprising antibodies or the BPIs from the
CC present invention can be used for screening, diagnosing or determining
CC the stage or severity of breast cancer, identifying a subject at risk of
CC developing breast cancer, or monitoring the effect of therapy
CC administered to a subject with breast cancer. The antibodies, BPIs,
CC nucleic acids encoding the BPIs, or an agent that modulates the activity
CC of one or more BPIs are useful for treating or preventing breast cancer.
CC ABP57104 to ABP57250 represent breast cancer associated tryptic digest
CC peptides, which are used in the exemplification of the present invention
XX
SQ Sequence 16 AA;

Query Match 44.3%; Score 89; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EQLGPVTQEFWDNLEK 27
Db 1 EQLGPVTQEFWDNLEK 16

RESULT 2
AAG62607
ID AAG62607 standard; peptide; 16 AA.

XX AAG62607;

XX 06-SEP-2001 (first entry)

DE Apolipoprotein fragment #1.

KW Apolipoprotein; ApoA-1; atherosclerosis; coronary disease;
KW cardiovascular disease; ischaemic heart disease; dyslipidaemia.

OS Unidentified.

FH Key Location/Qualifiers

FT Modified-site 14
FT /label= OTHER
FT /note= "optionally oxidised"

XX WO200138395-A1.

PN 31-MAY-2001.

PD 27-NOV-2000; 2000WO-AU001463.

XX 26-NOV-1999; 99AU-00004293.

XX (HEAR-) HEART RES INST LTD.

PI Stocker R, Wang XL, Wilcken D;

XX WPI; 2001-355909/37.

XX Novel oxidized form of apolipoprotein useful in diagnosis and treatment
PT of diseases associated with oxidative stress such as cardiovascular
PT diseases, in particular, atherosclerosis.

PS Example 1; Page 28; 55pp; English.

XX The present invention relates to oxidised apolipoprotein A-I (ApoA-I)
CC where at least Met residue 86 is oxidised to Met(O). This can be used in
CC the prevention, diagnosis and treatment of lipid associated disorders,

CC including coronary vascular disease, ischaemic heart disease,
CC atherosclerosis and dyslipidaemias. The present sequence is a fragment of
CC the ApoA-I protein isolated in the exemplification of the invention
XX Sequence 16 AA;
SQ Query Match 39.8%; Score 80; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 DNLEKETEGLRQEMSK 38
Db 1 DNLEKETEGLRQEMSK 16

RESULT 3
AAE02141
ID AAE02141 standard; peptide; 37 AA.

XX AAE02141;

XX 31-JUL-2001 (first entry)

XX Mouse alpha helical protein-34 (Zalpha34) antigenic epitope #12.

KW Mouse; alpha helical protein-34; Zalpha34; antiinfertility;
KW antigenic epitope; spermatogenesis; educational kit; therapy;
KW tumour associated antigen.

OS Mus musculus.

XX WO200132884-A2.

XX 10-MAY-2001.

XX 24-OCT-2000; 2000WO-US029277.

XX 29-OCT-1999; 99US-00430153.

XX (ZYMO) ZYMOGENETICS INC.

XX Conklin DC, Taft DW;

XX WPI; 2001-316446/33.

XX Educational kit useful for courses related to genetics, molecular
PT biology, protein chemistry, antibody production and analysis, has a
PT container having novel alpha helical protein-34 polypeptide or
PT polynucleotide.

PS Claim 9; Page 66; 77pp; English.

XX The present sequence is mouse alpha helical protein-34 (Zalpha34)
CC antigenic epitope. Zalpha34 polynucleotides, polypeptides and antibodies
CC are useful as educational tools, as a laboratory practicum kits for
CC courses related to genetics and molecular biology, protein chemistry and
CC antibody production and analysis. Zalpha34 is useful for promoting
CC spermatogenesis, to identify inhibitors of its activity and to prepare
CC antibodies that specifically binds to Zalpha34 groups, peptides or
CC polypeptides. The antibodies are useful for inhibiting spermatogenesis
CC and to isolate DNA sequences that encode human Zalpha34 genes from cDNA
CC libraries. Zalpha34 polypeptides are useful as an aid to teach
CC preparation of antibodies, identifying proteins by western blotting,
CC protein purification and determining the weight of expressed Zalpha34
CC polypeptides as a ratio to total protein expressed. Fusion proteins
CC comprising Zalpha34 and a Fc group are useful as an in vitro assay tool
CC and antibody-Zalpha34 fusion comprising antibody variable domains are
CC useful as therapeutic proteins, in which the antibody group binds with
CC the target antigen, such as a tumour associated antigen

XX Sequence 37 AA;

XX Query Match 30.1%; Score 60.5; DB 4; Length 37;

| | | | |
|---|---|---|--|
| Best Local Similarity 54.2%; Pred. No. 1.8; | | Matches 13; Conservative 4; Mismatches 6; Indels 1; Gaps 1; | |
| QY | 12 EQLGPVTQEFWDNLEKETEGLRQE 35 : | | |
| Db | 1 EELGE-AQTVDNLQKELDLLREE 23 | | |
| RESULT 4 | | | |
| AAU99633 | AAU99633 standard; peptide; 37 AA. | | |
| XX | AAU99633; | | |
| DT | 07-OCT-2002 (first entry) | | |
| XX | Mouse secreted alpha protein 34, Zalpha34, epitope #12. | | |
| KW | Mouse; secreted alpha protein 34; Zalpha34; epitope; immunogen; | | |
| KW | chromosome 7; spermatogenesis; hormonal; cytokine; teaching aid; | | |
| KW | protein chemistry; enzyme-linked immunoabsorbent assay; ELISA. | | |
| OS | Mus musculus. | | |
| XX | US6380361-B1. | | |
| PN | 30-APR-2002. | | |
| XX | 24-OCT-2000; 2000US-00695458. | | |
| PF | 29-OCT-1999; 99US-0162623P. | | |
| PR | (ZYMO) ZYMOGENETICS INC. | | |
| XX | Conklin DC, Taft DW; | | |
| PI | WPI; 2002-526165/56. | | |
| XX | Educational kits and aid for teaching protein chemistry comprising the | | |
| PT | isolated hormonal/cytokine cytokine alpha helical protein-34 (Z alpha 34) | | |
| PT | polypeptide, useful for teaching e.g. ELISA techniques and | | |
| PT | immunopurification. | | |
| PS | Disclosure; Col 51-52; 35pp; English. | | |
| XX | The invention relates to an educational kit or aid for teaching protein | | |
| CC | chemistry comprising a container having the isolated, novel hormonal/ | | |
| CC | cytokine alpha helical protein-34 (secreted protein alpha, Zalpha34) | | |
| CC | polypeptide, comprising defined amino acid sequences (AAU99639-AAU99654) | | |
| CC | given in the specification and/or the isolated polypeptides comprising | | |
| CC | (AAU99639-AAU99654). The educational kit or teaching aid may be used to | | |
| CC | teach protein chemistry. A novel full-length Zalpha34 protein can be used | | |
| CC | so the student can have practical learning experiences in protein | | |
| CC | purification procedures, protein re-folding when the protein is produced | | |
| CC | in prokaryotic host cells, and how to make both monoclonal and polyclonal | | |
| CC | antibodies. Antibodies that bind to mature Zalpha34 proteins can also be | | |
| CC | used to learn how to make affinity purification columns, to do enzyme- | | |
| CC | linked immunoabsorbent assays (ELISA). The mouse gene encoding Zalpha34 | | |
| CC | is located on chromosome 7. Zalpha34 is useful for promoting | | |
| CC | spermatogenesis. The present sequence is an immunogenic epitope from the | | |
| CC | mouse Zalpha34 protein | | |
| XX | | | |
| SQ | Sequence 37 AA; | | |
| Query Match 30.1%; Score 60.5; DB 5; Length 37; | | Best Local Similarity 54.2%; Pred. No. 1.8; | |
| Matches 13; Conservative 4; Mismatches 6; Indels 1; Gaps 1; | | | |
| QY | 12 EQLGPVTQEFWDNLEKETEGLRQE 35 : | | |
| Db | 1 EELGE-AQTVDNLQKELDLLREE 23 | | |

| | | | |
|--|---|---|--|
| RESULT 5 | | AAY18752 standard; peptide; 22 AA. | |
| ID | AAY18752 | | |
| XX | AAY18752; | | |
| AC | 09-JUL-1999 (first entry) | | |
| XX | Lecithin:cholesterol acyltransferase activation exhibiting peptide #73. | | |
| DE | Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human; | | |
| XX | lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia; | | |
| KW | cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I; | | |
| KW | high density lipoprotein; hypertriglyceridemia; metabolic syndrome; | | |
| KW | septic shock. | | |
| XX | Synthetic. | | |
| OS | Homo sapiens. | | |
| XX | WO9916408-A2. | | |
| PN | 08-APR-1999. | | |
| XX | 28-SEP-1998; 98WO-US020328. | | |
| PF | 29-SEP-1997; 97US-00940093. | | |
| XX | (DASS/) DASSEUX J. | | |
| PA | (SEKU/) SEKUL R. | | |
| PA | (BUTT/) BUTTNER K. | | |
| PA | (CORN/) CORNUT I. | | |
| PA | (METZ/) METZ G. | | |
| XX | Dasseux J, Sekul R, Buttner K, Cornut I, Metz G; | | |
| PI | WPI; 1999-277031/23. | | |
| DR | Peptide agonists of apolipoprotein A-I. | | |
| XX | Example; Page 107; 152pp; English. | | |
| PT | The present invention describes an agonist (A) of apolipoprotein A-I | | |
| CC | (apoA-I) which is a 14-22 residue peptide, or analog, that forms an | | |
| CC | amphipathic alpha-helix in presence of lipids. (A), and their lipid | | |
| CC | complexes, are used to treat or prevent diseases associated with | | |
| CC | dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, | | |
| CC | atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I | | |
| CC | deficiency; hypertriglyceridemia and metabolic syndrome, also for | | |
| CC | treating septic shock. When labeled, (A) can also be used diagnostically | | |
| CC | to measure serum levels of HDL, in particular the HDL subpopulation that | | |
| CC | is involved in retrograde cholesterol transport, also to image HDL at | | |
| CC | e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to | | |
| CC | AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity | | |
| CC | exhibiting core peptides, which are apoA-I agonists | | |
| XX | | | |
| SQ | Sequence 22 AA; | | |
| Query Match 27.9%; Score 56; DB 2; Length 22; | | Best Local Similarity 42.9%; Pred. No. 3.9; | |
| Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0; | | | |
| QY | 16 PVTQEFWDNLEKETEGLRQEM 36 | | |
| Db | 1 PVLDFWEKLNEXLEALKQKL 21 | | |
| RESULT 6 | | | |
| AA19006 | AA19006 standard; peptide; 22 AA. | | |
| ID | AA19006 | | |
| XX | AA19006; | | |
| AC | 09-JUL-1999 (first entry) | | |
| XX | | | |
| DT | | | |

XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #73.
XX OS
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX OS Synthetic.
OS Homo sapiens.
XX WO9916458-A1.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-US020326.
XX PP 29-SEP-1997; 97US-00940096.
XX PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G;
XX WPI; 1999-277034/23.
DR Peptide agonists of apolipoprotein A-I.
XX Example; Page 110; 254pp; English.
XX CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
CC AAY19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX SQ Sequence 22 AA;
Query Match 27.9%; Score 56; DB 2; Length 22;
Best Local Similarity 42.9%; Pred. No. 3.9;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Qy 16 PVTQEFWDNLEKETEGLRQEM 36
Db 1 PVLDEFWEKLNEXLEALKQKL 21
RESULT 7
AAY19260
ID AAY19260 standard; peptide; 22 AA.
XX AC AAY19260;
XX 14-JUL-1999 (first entry)
XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #73.
XX Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;

KW septic shock.
XX Synthetic.
OS Homo sapiens.
XX WO9916459-A1.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-US020327.
XX PP 29-SEP-1997; 97US-00940095.
XX PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX WPI; 1999-277035/23.
DR Peptide agonists of apolipoprotein A-I.
XX Example; Page 119; 280pp; English.
XX CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX SQ Sequence 22 AA;
Query Match 27.9%; Score 56; DB 2; Length 22;
Best Local Similarity 42.9%; Pred. No. 3.9;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Qy 16 PVTQEFWDNLEKETEGLRQEM 36
Db 1 PVLDEFWEKLNEXLEALKQKL 21
RESULT 8
AAY18489
ID AAY18489 standard; peptide; 22 AA.
XX AC AAY18489;
XX 09-JUL-1999 (first entry)
XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #73.
XX Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder; ApoA-I;
KW cardiovascular disease; atherosclerosis; restenosis; LCAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
XX Synthetic.
OS Homo sapiens.
XX WO9916409-A2.
XX PD 08-APR-1999.

XX 28-SEP-1998; 98WO-US020329.
PF (SEKU/) SEKUL R.
XX (BUTT/) BUTTNER K.
PR (CORN/) CORNUT I.
XX (METZ/) METZ G.
XX (DUFO/) DUFOURCQ J.
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
PI WPI; 1999-254921/21.
XX Nucleic acid encoding apoproteinA-I agonist peptides.
XX Example; Page 148; 232pp; English.
XX The present invention describes a nucleic acid (A) encoding an
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
CC which forms an amphipathic alpha-helix in presence of lipids. (A),
CC optionally as a complex with lipids, and host cells that contain (A), are
CC useful for gene therapy, or prevention, of diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
CC endotoxemia (septic shock). Host cells containing (A) can also be used to
CC study the role of apoA-I in lipid metabolism. (B) can be used
CC diagnostically, e.g. to measure serum HDL (particularly its subpopulation
CC involved in retrograde cholesterol transport) and for imaging the
CC circulatory system or HDL accumulations at fatty streaks. The present
CC sequence represents a peptide from the present invention
XX
SQ Sequence 22 AA;
Query Match 27.9%; Score 56; DB 2; Length 22;
Best Local Similarity 42.9%; Pred. No. 3.9;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 16 PVTQEFWDNLEKETEGLRQEM 36
Db || |||: | : | |::
1 PVLDEFWEKLNEXLEALKQKL 21
RESULT 9
ADG20969
ID ADG20969 standard; peptide; 22 AA.
XX
AC ADG20969;
XX
DT 26-FEB-2004 (first entry)
XX
DE Apolipoprotein A-I agonist peptide seq id 73.
XX
KW apolipoprotein A-I; ApoA-I; agonist; peptide analogue;
KW amphipathic alpha-helix; dyslipidaemia; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis;
KW high density lipoprotein; HDL; Apia-I deficiency; hypertriglyceridaemia;
KW metabolic syndrome; septic shock.
XX
OS Synthetic.
XX
XX US2003203842-A1.
PN 30-OCT-2003.
PD
XX
XX 15-MAR-2002; 2002US-00099836.
PF
XX
PR 01-DEC-1999; 99US-00453834.
XX
PA (DASS/) DASSEUX J.

PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
PI WPI; 2004-010524/01.
XX
PT Novel apolipoprotein agonist treating subject suffering from disorder
PT associated with dyslipidemia such as hypercholesterolemia, cardiovascular
PT disease, atherosclerosis, restenosis, hypertriglyceridemia or metabolic
PT syndrome.
XX
PS Claim 19; SEQ ID NO 73; 146pp; English.
XX
CC The invention describes an apolipoprotein A-I (ApoA-I) agonist (A)
CC comprising a 15-29 residue peptide or peptide analogue which forms an
CC amphipathic alpha-helix in the presence of lipids or its salt. (A) is
CC useful for treating a subject suffering from a disorder associated with
CC dyslipidaemia (hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, high density lipoprotein (HDL) or Apia-I
CC deficiency, hypertriglyceridaemia or metabolic syndrome) or septic shock.
CC This is the amino acid sequence of a ApoA-I agonist peptide.
XX
SQ Sequence 22 AA;
Query Match 27.9%; Score 56; DB 8; Length 22;
Best Local Similarity 42.9%; Pred. No. 3.9;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 16 PVTQEFWDNLEKETEGLRQEM 36
Db || |||: | : | |::
1 PVLDEFWEKLNEXLEALKQKL 21
RESULT 10
ADJ32911
ID ADJ32911 standard; peptide; 22 AA.
XX
AC ADJ32911;
XX
DT 22-APR-2004 (first entry)
XX
DE Apo lipoprotein A-I (ApoA-I) agonist peptide #73.
XX
KW Apo lipoprotein A-I agonist; ApoA-I agonist; amphipathic alpha-helix;
KW dyslipidaemia; hypercholesterolaemia; cardiovascular disease;
KW atherosclerosis; restenosis; high density lipoprotein deficiency;
KW HDL deficiency; ApoA-I deficiency; hypertriglyceridaemia;
KW metabolic syndrome; septic shock; coronary heart disease; endotoxaemia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 13 /label= Aib
FT
XX US2003060604-A1.
PN 27-MAR-2003.
PD
XX
PF 15-MAR-2002; 2002US-00099574.
XX
PR 17-DEC-1999; 99US-00465718.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX

Db |||||
 8 DSVTSTFSKLR 18

RESULT 13
ADC29658
ID ADC29658 standard; peptide; 18 AA.
XX
AC ADC29658;
XX
DT 18-DEC-2003 (first entry)
XX
DE Antioxidant peptide #33.
XX
KW antioxidant; cardiovascular disease; ischaemia; bone disease;
KW inflammatory related disease; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003087819-A1.
XX
PD 08-MAY-2003.
XX
PF 08-MAY-2002; 2002US-00142238.
XX
PR 09-MAY-2001; 2001US-0289944P.
XX
PA (BIEL/) BIELICKI J K.
XX
PI Bielicki JK;
XX
DR WPI; 2003-786946/74.
XX
PT New cysteine-containing peptides, having antioxidant properties, useful
PT for diagnosing and treating cardiovascular disease, ischemia, bone
PT disease and other inflammatory related diseases.
XX
PS Synthetic.
OS Homo sapiens.
XX
PN US2003087819-A1.
XX
PD 08-MAY-2003.
XX
PF 08-MAY-2002; 2002US-00142238.
XX
PR 09-MAY-2001; 2001US-0289944P.
XX
PA (BIEL/) BIELICKI J K.
XX
PI Bielicki JK;
XX
DR WPI; 2003-786946/74.
XX
PT New cysteine-containing peptides, having antioxidant properties, useful
PT for diagnosing and treating cardiovascular disease, ischemia, bone
PT disease and other inflammatory related diseases.
XX
PS Example 8; SEQ ID NO 33; 49pp; English.
XX
CC The invention relates to an antioxidant peptide. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating cardiovascular disease, ischaemia, bone disease and other
CC inflammatory related diseases. The present sequence represents the amino
CC acid sequence of a peptide with antioxidant activity.
XX
SQ Sequence 18 AA;

Query Match 25.9%; Score 52; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLR 11
 |||||
Db 8 DSVTSTFSKLR 18
 |||||

RESULT 14
ADC29661
ID ADC29661 standard; peptide; 18 AA.
XX
AC ADC29661;
XX
DT 18-DEC-2003 (first entry)
XX
DE Antioxidant peptide #36.
XX
KW antioxidant; cardiovascular disease; ischaemia; bone disease;
KW inflammatory related disease; human.
XX
OS Synthetic.
OS Homo sapiens.
XX

Query Match 25.9%; Score 52; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLR 11
 |||||
Db 8 DSVTSTFSKLR 18
 |||||

PN US2003087819-A1.
XX
PD 08-MAY-2003.
XX
PF 08-MAY-2002; 2002US-00142238.
XX
PR 09-MAY-2001; 2001US-0289944P.
XX
PA (BIEL/) BIELICKI J K.
XX
PI Bielicki JK;
XX
DR WPI; 2003-786946/74.
XX
PT New cysteine-containing peptides, having antioxidant properties, useful
PT for diagnosing and treating cardiovascular disease, ischemia, bone
PT disease and other inflammatory related diseases.
XX
PS Example 8; SEQ ID NO 36; 49pp; English.
XX
CC The invention relates to an antioxidant peptide. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating cardiovascular disease, ischaemia, bone disease and other
CC inflammatory related diseases. The present sequence represents the amino
CC acid sequence of a peptide with antioxidant activity.
XX
SQ Sequence 18 AA;

Query Match 25.9%; Score 52; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLR 11
 |||||
Db 8 DSVTSTFSKLR 18
 |||||

RESULT 15
ADC29657
ID ADC29657 standard; peptide; 18 AA.
XX
AC ADC29657;
XX
DT 18-DEC-2003 (first entry)
XX
DE Antioxidant peptide #32.
XX
KW antioxidant; cardiovascular disease; ischaemia; bone disease;
KW inflammatory related disease; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003087819-A1.
XX
PD 08-MAY-2003.
XX
PF 08-MAY-2002; 2002US-00142238.
XX
PR 09-MAY-2001; 2001US-0289944P.
XX
PA (BIEL/) BIELICKI J K.
XX
PI Bielicki JK;
XX
DR WPI; 2003-786946/74.
XX
PT New cysteine-containing peptides, having antioxidant properties, useful
PT for diagnosing and treating cardiovascular disease, ischemia, bone
PT disease and other inflammatory related diseases.
XX
PS Example 8; SEQ ID NO 32; 49pp; English.
XX

CC The invention relates to an antioxidant peptide. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating cardiovascular diseases, ischaemia, bone disease and other
CC inflammatory related diseases. The present sequence represents the amino
CC acid sequence of a peptide with antioxidant activity.

XX

SQ Sequence 18 AA;

Query Match 25.9%; Score 52; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLR 11

|||||

Db 8 DSVTSTFSKLR 18

Search completed: December 21, 2004, 12:21:51
Job time : 155 secs

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OM protein - protein search, using sw model

Run on: December 21, 2004, 11:55:11 ; Search time 142 Seconds
(without alignments)
98.279 Million cell updates/sec

Title: US-09-803-918A-2_COPY_75_113
Perfect score: 201
Sequence: 1 DSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 382105

Minimum DB seq length: 0
Maximum DB seq length: 41

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 118 | 58.7 | 22 | 15 | US-10-465-789A-50 |
| 2 | 89 | 44.3 | 16 | 17 | US-10-700-340-37 |
| 3 | 72 | 35.8 | 22 | 15 | US-10-465-789A-49 |
| 4 | 56 | 27.9 | 22 | 10 | US-09-865-989-73 |
| 5 | 56 | 27.9 | 22 | 11 | US-09-865-989-73 |
| 6 | 56 | 27.9 | 22 | 14 | US-10-099-574A-73 |
| 7 | 56 | 27.9 | 22 | 14 | US-10-147-849-73 |
| 8 | 56 | 27.9 | 22 | 14 | US-10-099-836B-73 |
| 9 | 56 | 27.9 | 22 | 14 | US-10-283-599-73 |
| 10 | 56 | 27.9 | 22 | 16 | US-10-802-080-73 |
| 11 | 56 | 27.9 | 22 | 17 | US-10-801-897-73 |
| 12 | 53 | 26.4 | 11 | 15 | US-10-465-789A-59 |
| 13 | 52 | 25.9 | 18 | 14 | US-10-142-238A-32 |

| | | | | | | |
|----|----|------|----|----|--------------------|-------------------|
| 14 | 52 | 25.9 | 18 | 14 | US-10-142-238A-33 | Sequence 33, Appl |
| 15 | 52 | 25.9 | 18 | 14 | US-10-142-238A-34 | Sequence 34, Appl |
| 16 | 52 | 25.9 | 18 | 14 | US-10-142-238A-35 | Sequence 35, Appl |
| 17 | 52 | 25.9 | 18 | 14 | US-10-142-238A-36 | Sequence 36, Appl |
| 18 | 52 | 25.9 | 18 | 14 | US-10-142-238A-37 | Sequence 37, Appl |
| 19 | 52 | 25.9 | 30 | 14 | US-10-142-238A-39 | Sequence 39, Appl |
| 20 | 52 | 25.9 | 30 | 14 | US-10-142-238A-40 | Sequence 40, Appl |
| 21 | 52 | 25.9 | 30 | 14 | US-10-142-238A-41 | Sequence 41, Appl |
| 22 | 52 | 25.9 | 30 | 14 | US-10-142-238A-42 | Sequence 42, Appl |
| 23 | 52 | 25.9 | 30 | 14 | US-10-142-238A-43 | Sequence 43, Appl |
| 24 | 52 | 25.9 | 30 | 14 | US-10-142-238A-44 | Sequence 44, Appl |
| 25 | 52 | 25.9 | 30 | 14 | US-10-142-238A-45 | Sequence 45, Appl |
| 26 | 50 | 24.9 | 10 | 10 | US-09-991-627-2 | Sequence 2, Appl |
| 27 | 48 | 23.9 | 22 | 10 | US-09-865-989-75 | Sequence 75, Appl |
| 28 | 48 | 23.9 | 22 | 11 | US-09-865-989-75 | Sequence 75, Appl |
| 29 | 48 | 23.9 | 22 | 14 | US-10-099-574A-75 | Sequence 75, Appl |
| 30 | 48 | 23.9 | 22 | 14 | US-10-147-849-75 | Sequence 75, Appl |
| 31 | 48 | 23.9 | 22 | 14 | US-10-099-836B-75 | Sequence 75, Appl |
| 32 | 48 | 23.9 | 22 | 14 | US-10-283-599-75 | Sequence 75, Appl |
| 33 | 48 | 23.9 | 22 | 16 | US-10-802-080-75 | Sequence 75, Appl |
| 34 | 48 | 23.9 | 22 | 17 | US-10-801-897-75 | Sequence 75, Appl |
| 35 | 47 | 23.4 | 22 | 10 | US-09-865-989-120 | Sequence 120, App |
| 36 | 47 | 23.4 | 22 | 11 | US-09-865-989-120 | Sequence 120, App |
| 37 | 47 | 23.4 | 22 | 14 | US-10-099-574A-120 | Sequence 120, App |
| 38 | 47 | 23.4 | 22 | 14 | US-10-147-849-120 | Sequence 120, App |
| 39 | 47 | 23.4 | 22 | 14 | US-10-099-836B-120 | Sequence 120, App |
| 40 | 47 | 23.4 | 22 | 14 | US-10-283-599-120 | Sequence 120, App |
| 41 | 47 | 23.4 | 22 | 16 | US-10-802-080-120 | Sequence 120, App |
| 42 | 47 | 23.4 | 22 | 17 | US-10-801-897-120 | Sequence 120, App |
| 43 | 46 | 22.9 | 22 | 10 | US-09-865-989-77 | Sequence 77, Appl |
| 44 | 46 | 22.9 | 22 | 10 | US-09-865-989-78 | Sequence 78, Appl |
| 45 | 46 | 22.9 | 22 | 10 | US-09-865-989-122 | Sequence 122, App |

ALIGNMENTS

RESULT 1
US-10-465-789A-50
; Sequence 50, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 50
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 2
US-10-465-789A-50

Query Match 58.7%; Score 118; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEMS 37
|||||
Db 1 PVTQEFWDNLEKETEGLRQEMS 22

RESULT 2
US-10-700-340-37
; Sequence 37, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Achula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREAST CANCER
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-37

Query Match 44.3%; Score 89; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EQLGPVTQEFWDNLEK 27
|||
Db 1 EQLGPVTQEFWDNLEK 16

RESULT 3
US-10-465-789A-49
; Sequence 49, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 1
US-10-465-789A-49

Query Match 35.8%; Score 72; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.018;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DSVTSTFSKLRQLG 15
|||
Db 8 DSVTSTFSKLRQLG 22

RESULT 4
US-09-865-989-73
; Sequence 73, Application US/09865989
; Publication No. US20030008827A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030008827A1e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-865-989-73

Query Match 27.9%; Score 56; DB 10; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 16 PVTQEFWDNLEKETEGLRQEM 36
|||
Db 1 PVLDFWEKLNEXLEALKQKL 21

RESULT 5
US-09-865-989-73
; Sequence 73, Application US/09865989

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; Publication No. US20040029807A9
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
;           Sekul, Renate
;           Buttner, Klaus
;           Cornut, Isabelle
;           Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;           AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 22 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: No. US20040029807A9e
; FEATURE:
;   NAME/KEY: Other
;   LOCATION: 13
;   OTHER INFORMATION: Xaa = Aib
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-865-989-73

Query Match      27.9%; Score 56; DB 11; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      16 PVTQEFWDNLEKETEGLRQEM 36
Db      1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 6
US-10-099-574A-73
; Sequence 73, Application US/10099574A
; Publication No. US20030060604A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,574A
; FILING DATE: 29-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 22 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: No. US20030060604A1e
; FEATURE:
;   NAME/KEY: Other
;   LOCATION: 13
;   OTHER INFORMATION: Xaa = Aib
; US-10-099-574A-73

Query Match      27.9%; Score 56; DB 14; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      16 PVTQEFWDNLEKETEGLRQEM 36
Db      1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 7
US-10-147-849-73
; Sequence 73, Application US/10147849
; Publication No. US20030190319A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,849
; FILING DATE: 29-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030190319A1e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
; US-10-147-849-73

Query Match 27.9%; Score 56; DB 14; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
||| | | | : | | | : | : | :
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 8

US-10-099-836B-73
; Sequence 73, Application US/10099836B
; Publication No. US20030203842A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,836B
; FILING DATE: 28-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030203842A1e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
; US-10-099-836B-73

Query Match 27.9%; Score 56; DB 14; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
||| | | | : | | | : | : | :
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 9

US-10-283-599-73
; Sequence 73, Application US/10283599
; Publication No. US20030208059A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:


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;
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030208059A1e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
;
US-10-283-599-73

Query Match      27.9%; Score 56; DB 14; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 10
US-10-802-080-73
; Sequence 73, Application US/10802080
; Publication No. US20040181034A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
;
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSGLIPIDEMIC DISORDERS
;
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/802,080
; FILING DATE: 15-Mar-2004
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE: 01-DEC-1999
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
;
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
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; OTHER INFORMATION: Xaa = Aib
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-10-802-080-73

Query Match      27.9%; Score 56; DB 16; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 11
US-10-801-897-73
; Sequence 73, Application US/10801897
; Publication No. US20040198662A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
;
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSGLIPIDEMIC DISORDERS
;
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/801,897
; FILING DATE: 15-Mar-2004
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
;
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
;
US-10-801-897-73

Query Match      27.9%; Score 56; DB 17; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
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Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 12
US-10-465-789A-59
; Sequence 59, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 0.5
US-10-465-789A-59

Query Match 26.4%; Score 53; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 STFSKLRQLG 15
Db 1 STFSKLRQLG 11

RESULT 13
US-10-142-238A-32
; Sequence 32, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-32

Query Match 25.9%; Score 52; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLR 11
Db 8 DSVTSTFSKLR 18

RESULT 14
US-10-142-238A-33
; Sequence 33, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-33

Query Match 25.9%; Score 52; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLR 11
Db 8 DSVTSTFSKLR 18

RESULT 15
US-10-142-238A-34
; Sequence 34, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-34

Query Match 25.9%; Score 52; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLR 11
Db 8 DSVTSTFSKLR 18

Search completed: December 21, 2004, 12:04:53
Job time : 143 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 11:59:59 ; Search time 37 Seconds
(without alignments)
69.903 Million cell updates/sec

Title: US-09-803-918A-2_COPY_75_113
 Perfect score: 201
 Sequence: 1 DSVTSTFSKLRQLGCPVTOEFWDNLEKETEGLRQEMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 251498

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Minimum DB seq length: 0
Maximum DB seq length: 41
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | | Length | DB | ID | Description |
|------------|-------|---------|----|--------|------------------|-------------------|-------------|
| | | Match | | | | | |
| 1 | 60.5 | 30.1 | 37 | 3 | US-09-695-458-15 | Sequence 15, Appl | |
| 2 | 56 | 27.9 | 22 | 3 | US-08-940-095-73 | Sequence 73, Appl | |
| 3 | 56 | 27.9 | 22 | 3 | US-08-940-093-73 | Sequence 73, Appl | |
| 4 | 56 | 27.9 | 22 | 3 | US-08-940-096-73 | Sequence 73, Appl | |
| 5 | 56 | 27.9 | 22 | 3 | US-09-465-719-73 | Sequence 73, Appl | |
| 6 | 56 | 27.9 | 22 | 3 | US-09-453-605-73 | Sequence 73, Appl | |
| 7 | 56 | 27.9 | 22 | 3 | US-09-453-838-73 | Sequence 73, Appl | |
| 8 | 56 | 27.9 | 22 | 4 | US-08-940-136-73 | Sequence 73, Appl | |
| 9 | 56 | 27.9 | 22 | 4 | US-09-453-841-73 | Sequence 73, Appl | |
| 10 | 56 | 27.9 | 22 | 4 | US-09-453-833-73 | Sequence 73, Appl | |
| 11 | 56 | 27.9 | 22 | 4 | US-09-453-826-73 | Sequence 73, Appl | |
| 12 | 56 | 27.9 | 22 | 4 | US-09-453-840-73 | Sequence 73, Appl | |
| 13 | 56 | 27.9 | 22 | 4 | US-09-865-989-73 | Sequence 73, Appl | |
| 14 | 56 | 27.9 | 22 | 4 | US-09-453-834-73 | Sequence 73, Appl | |
| 15 | 51 | 25.4 | 22 | 1 | US-07-928-930A-8 | Sequence 8, Appli | |
| 16 | 51 | 25.4 | 22 | 1 | US-08-288-568-8 | Sequence 8, Appli | |
| 17 | 51 | 25.4 | 22 | 1 | US-08-487-461-8 | Sequence 8, Appli | |
| 18 | 51 | 25.4 | 22 | 1 | US-08-432-691-8 | Sequence 8, Appli | |
| 19 | 51 | 25.4 | 22 | 1 | US-08-487-459-8 | Sequence 8, Appli | |
| 20 | 48 | 23.9 | 22 | 3 | US-08-940-095-75 | Sequence 75, Appl | |
| 21 | 48 | 23.9 | 22 | 3 | US-08-940-093-75 | Sequence 75, Appl | |
| 22 | 48 | 23.9 | 22 | 3 | US-08-940-096-75 | Sequence 75, Appl | |
| 23 | 48 | 23.9 | 22 | 3 | US-09-465-719-75 | Sequence 75, Appl | |
| 24 | 48 | 23.9 | 22 | 3 | US-09-453-605-75 | Sequence 75, Appl | |
| 25 | 48 | 23.9 | 22 | 3 | US-09-453-838-75 | Sequence 75, Appl | |
| 26 | 48 | 23.9 | 22 | 4 | US-08-940-136-75 | Sequence 75, Appl | |
| 27 | 48 | 23.9 | 22 | 4 | US-09-453-841-75 | Sequence 75, Appl | |

| | | | | | | |
|----|----|------|----|---|-------------------|-------------------|
| 28 | 48 | 23.9 | 22 | 4 | US-09-453-833-75 | Sequence 75, Appl |
| 29 | 48 | 23.9 | 22 | 4 | US-09-453-826-75 | Sequence 75, Appl |
| 30 | 48 | 23.9 | 22 | 4 | US-09-453-840-75 | Sequence 75, Appl |
| 31 | 48 | 23.9 | 22 | 4 | US-09-865-989-75 | Sequence 75, Appl |
| 32 | 48 | 23.9 | 22 | 4 | US-09-453-834-75 | Sequence 75, Appl |
| 33 | 47 | 23.4 | 22 | 3 | US-08-940-095-120 | Sequence 120, App |
| 34 | 47 | 23.4 | 22 | 3 | US-08-940-093-120 | Sequence 120, App |
| 35 | 47 | 23.4 | 22 | 3 | US-08-940-096-120 | Sequence 120, App |
| 36 | 47 | 23.4 | 22 | 3 | US-09-465-719-120 | Sequence 120, App |
| 37 | 47 | 23.4 | 22 | 3 | US-09-453-605-120 | Sequence 120, App |
| 38 | 47 | 23.4 | 22 | 3 | US-09-453-838-120 | Sequence 120, App |
| 39 | 47 | 23.4 | 22 | 4 | US-08-940-136-120 | Sequence 120, App |
| 40 | 47 | 23.4 | 22 | 4 | US-09-453-841-120 | Sequence 120, App |
| 41 | 47 | 23.4 | 22 | 4 | US-09-453-833-120 | Sequence 120, App |
| 42 | 47 | 23.4 | 22 | 4 | US-09-453-826-120 | Sequence 120, App |
| 43 | 47 | 23.4 | 22 | 4 | US-09-453-840-120 | Sequence 120, App |
| 44 | 47 | 23.4 | 22 | 4 | US-09-865-989-120 | Sequence 120, App |
| 45 | 47 | 23.4 | 22 | 4 | US-09-453-834-120 | Sequence 120, App |

ALIGNMENTS

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RESULT 1
US-09-695-458-15
; Sequence 15, Application US/09695458
; Patent No. 6380361
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: Educational Kit and M
; TITLE OF INVENTION: Protein-34
; FILE REFERENCE: 99-78
; CURRENT APPLICATION NUMBER: US/09/695,458
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/162,623
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-695-458-15

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Query Match          30.1%; Score 60.5; DB 3; Length 37;
Best Local Similarity 54.2%; Pred. No. 0.27;
Matches 13; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

y      12 EQLGPVTQEFWDNLEKETEGLRQE 35
      ||| | |||:| | : ||:|
b      1 EELGE-AQTVDNLQKELDLLREE 23

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RESULT 2
US-08-940-095-73
; Sequence 73, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

```

; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
;
; US-08-940-095-73
;
Query Match 27.9%; Score 56; DB 3; Length 22;
Best local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
   ||| ||| : | : | : | :
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 3
US-08-940-093-73
; Sequence 73, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435

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; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
US-08-940-096-73

Query Match      27.9%; Score 56; DB 3; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      16 PVTQEFWDNLEKETEGLRQEM 36
Db      1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 5
US-09-465-719-73
; Sequence 73, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib

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US-09-465-719-73

Query Match      27.9%; Score 56; DB 3; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      16 PVTQEFWDNLEKETEGLRQEM 36
Db      1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 6
US-09-453-605-73
; Sequence 73, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-No. 6329341-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-453-605-73

Query Match      27.9%; Score 56; DB 3; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      16 PVTQEFWDNLEKETEGLRQEM 36
Db      1 PVLDEFWEKLNEXLEALKQKL 21

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RESULT 7
US-09-453-838-73
; Sequence 73, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
US-09-453-838-73

Query Match 27.9%; Score 56; DB 3; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
|||::|:|::|:
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 8
US-08-940-136-73
; Sequence 73, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
```

```
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
US-08-940-136-73

Query Match 27.9%; Score 56; DB 4; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGLRQEM 36
|||::|:|::|:
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 9
US-09-453-841-73
; Sequence 73, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
```

;
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
; US-09-453-841-73

Query Match 27.9%; Score 56; DB 4; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 16 PVTQEFWDNLEKETEGLRQEM 36
|| |||:|:|:|:|:|:|:|:|:|:
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 10
US-09-453-833-73
; Sequence 73, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:

;
; APPLICATION NUMBER: US/09/453,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6602854e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
; US-09-453-833-73

Query Match 27.9%; Score 56; DB 4; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 16 PVTQEFWDNLEKETEGLRQEM 36
|| |||:|:|:|:|:|:|:|:|:|:
Db 1 PVLDEFWEKLNEXLEALKQKL 21

RESULT 11
US-09-453-826-73
; Sequence 73, Application US/09453826
; Patent No. 6630450
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,826
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999

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;
STRANDEDNESS: single
;
TOPOLOGY: linear
;

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Query Match 27.9%; Score 56; DB 4; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels

Qy 16 PVTQEFWDNLEKETETGLRQEM 36
 || ||| : | : | :
Dd 1 PVLDEFWEKLNEXLEALKOKL 21

RESULT 14

US-09-453-834-73
; Sequence 73, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
;

| | | | | |
|-------------------------|--------|-----------------|-----------|------------|
| Query Match | 27.9%; | Score 56; | DB 4; | Length 22; |
| Best Local Similarity | 42.9%; | Pred. No. 0.58; | | |
| Matches 9; Conservative | 5; | Mismatches 7; | Indels 0; | Gaps 0; |

Qy 16 PVTQEFWDNLEKETETGLRQEM 36
 || ||| : | : : :
 Db 1 PVLDEFWEKLNEXLEALKOKL 21

RESULT 15

US-07-928-930A-8
; Sequence 8, Application US/07928930A
; Patent No. 5344822

; GENERAL INFORMATION:
 ; APPLICANT: Levine, Daniel M.; Parker, Thomas S.;
 ; APPLICANT: Rubin, Albert L.
 ; TITLE OF INVENTION: Methods Useful in Endotoxin
 ; TITLE OF INVENTION: Prophylaxis and Therapy
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ;

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,930A
FILING DATE: 19920812
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5344822man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: ROGO 206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-928-930A-8

Query Match 25.4%; Score 51; DB 1; Length 22;
Best Local Similarity 47.6%; Pred. No. 2.7;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 16 PVTQEFWDNLEKETETGLRQEM 36
Db 1 PVLDEFREKLNEELEALKOKM 21

Search completed: December 21, 2004, 12:15:07
Job time : 40 secs

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A; Cross-references: GB:W73486; NID:G204311; PIDN:AAA41220.1; PID:G204312
R; Srivastava, C.H.; Monts, B.S.; Rothrock, J.K.; Peredo, M.J.; Pescovitz, O.H.
Endocrinology 136, 1502-1508, 1995
A; Title: Presence of a spermatogenic-specific promoter in the rat growth hormone-release
A; Reference number: I53290; MUID:95203210; PMID:7895659

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-104 <RES>
A;Cross-references: EMBL:U10156; NID:g498584; PIDN:AAC52184.1; PID:g498585
C;Genetics:
A;Gene: GHRH
C;Superfamily: glucagon
C;Keywords: duplication

| | | | | |
|-----------------------|------------------|----------------|-----------|-------------|
| Query Match | 12.0% | Score 66.5; | DB 2; | Length 104; |
| Best Local Similarity | 32.9% | Pred. No. 86; | | |
| Matches 23; | Conservative 10; | Mismatches 32; | Indels 5; | Gaps 3; |

| | | | | | | |
|----------------|----|---|---------------|---------------------|-----------------------|----|
| Qy | 20 | RARHVDA | LRLTHLAPYSDEL | RQRLAARL--EALKENGGA | RLAEYHAKATEHLSTL-SEKA | 76 |
| | | : | : | : | : | |
| D _b | 27 | RVRRHADAIFT--SSYRILGOLYARKLLHEIMNRQOGERNOQRSFRNRLHLDRVWAEDK | 84 | | | |
| | | : | : | : | : | |
| Qy | 77 | KPALEDLRQG | 86 | | | |
| | | : : | : | | | |
| D _b | 85 | OMALESILOG | 94 | | | |

RESULT 3
H87560
conserved hypothetical protein CC2513 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87560
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon-
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87560
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <STO>
A;Cross-references: UNIPROT:Q9A5D7; GB:AE005673; NID:g13424070; PIDN:AAK24484.1; GSPDB:G
C;Genetics:
A;Gene: CC2513

RESULT 4
IWBO
ATPase inhibitor precursor, mitochondrial - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Feb-1984 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: C27382; A01336
R;Walker, J.E.; Gay, N.J.; Powell, S.J.; Kostina, M.; Dyer, M.R.
Biochemistry 26, 8613-8619, 1987
A;Title: ATP synthase from bovine mitochondria: sequences of imported precursors of olig
A;Reference number: A90527; MUID:88163536; PMID:2894843
A;Accession: C27382
A;Molecule type: mRNA
A;Residues: 1-109 <WAL>
A;Cross-references: UNIPROT:P01096; GB:M22559; NID:g162712; PIDN:AAA30396.1; PID:g162713
R;Frangione, B.; Rosenwasser, E.; Penefsky, H.S.; Pullman, M.E.
Proc. Natl. Acad. Sci. U.S.A. 78, 7403-7407, 1981

A:Title: Amino acid sequence of the protein inhibitor of mitochondrial adenosine triphosph
A:Reference number: A01336; MUID:82150878; PMID:6461003
A:Accession: A01336
A:Molecule type: protein
A:Residues: 26-54,'Q',56-109 <FRA>
A:Note: there are several internal duplications near the carboxyl end (residues 73-97)
C:Comment: This peptide is thought to be a regulatory component of the ATP-synthesizing
C:Superfamily: ATPase inhibitor, mitochondrial
C:Keywords: ATPase inhibitor; mitochondrion
F:1-25/Domain: transit peptide (mitochondrion) #status predicted <SIG>
F:26-109/Product: ATPase inhibitor #status experimental <MAT>

RESULT 5
T46234
hypothetical protein T9C5.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46234
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23026
A:Accession: T46234
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <RIE>
A:Cross-references: UNIPROT:Q9SCK2; EMBL:AL132964
A:Experimental source: cultivar Columbia; BAC clone T9C5
C:Genetics:
A:Map position: 3
A>Note: T9C5.160

RESULT 6
S76457
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C.Species: Synechocystis sp.
A.Variety: PCC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C.Accession: S76457
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud-
DNA Res. 3, 109-136, 1996
A.Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A.Reference number: S74322; MUID:97061201; PMID:8905231
A.Accession: S76457
A.Status: preliminary
A.Molecule type: DNA

A;Residues: 1-107 <KAN>
A;Cross-references: UNIPROT:P74485; EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA1858
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 11.2%; Score 62; DB 2; Length 107;
Best Local Similarity 23.9%; Pred. No. 2e+02;
Matches 21; Conservative 17; Mismatches 30; Indels 20; Gaps 3;

QY 7 QEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLA-----ARLEALKENGGARLA 59
Db 15 QEK-----EAYKEKVRAKIDKLNQAIQDMTAEAREKAADANVNYQKSLKDLQAQRDALMG 69

QY 60 EYHAKATEHLSTLSEKAKPALEDLRQGL 87
Db 70 KWH-----DLQSQGEAAWEELQAGL 89

RESULT 7
AI2730
transcription regulator, ArsR family Atu1254 [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI2730
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenthner, D.; Kutyaivin, T.; Levy, R.; Li, M.; McClellan Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104 <KUR>
A;Cross-references: UNIPROT:Q8UFZ0; GB:AE008688; PIDN:AAL42263.1; PID:g17739660; GSPDB: C;Genetics:
A;Gene: Atu1254
A;Map position: circular chromosome

Query Match 11.0%; Score 61; DB 2; Length 104;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 20; Conservative 10; Mismatches 23; Indels 12; Gaps 3;

QY 33 APYSDELRLQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLR---QGLLP 89
Db 46 APCQDMPRSTLSSHMRILREAG---LIRTHKQGVENISVV-----RLDMEARFPGLLP 96

QY 90 VLESF 94
Db 97 SILKF 101

RESULT 8
A59010
antifreeze protein LS-12 - longhorn sculpin
C;Species: Myoxocephalus octodecimspinosus (longhorn sculpin)
C;Date: 10-Oct-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
C;Accession: A59010
R;Deng, G.; Andrews, D.W.; Laursen, R.A.
FEBS Lett. 402, 17-20, 1997
A;Reference number: A59010; MUID:97165956; PMID:9013849
A;Accession: A59010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-108 <LAU>
A;Cross-references: UNIPROT:P80961
A;Experimental source: blood plasma
C;Keywords: antifreeze; plasma; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 11.0%; Score 61; DB 2; Length 108;

Best Local Similarity 22.9%; Pred. No. 2.5e+02;
Matches 25; Conservative 24; Mismatches 42; Indels 18; Gaps 4;

QY 10 LSPGLGEEMRDRARAHVDALRTHLAPYSDEL--RQRLAARLEALKENGGARLAEYHAKATE 67
Db 6 LESLGQ-----YFEEMKTKLIQDMTEIIRSQDLANQAQAFVEDKKTQLQPLVAQIQE 57

QY 68 HLSTLS-----EKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 112
Db 58 QMKT VATNVEEQIRPLTANVQAHLPQIDNFQ----KQMEAIKKLTDQ 102

RESULT 9
AB1439
small heat shock protein of Clostridium acetobutylicum homolog lin0049 [imported] - Lis. C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1439
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1439
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <GLA>
A;Cross-references: UNIPROT:Q92FQ4; GB:AL592022; PIDN:CAC95282.1; PID:g16412470; GSPDB: A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0049

Query Match 10.7%; Score 59.5; DB 2; Length 97;
Best Local Similarity 25.3%; Pred. No. 2.9e+02;
Matches 24; Conservative 20; Mismatches 30; Indels 21; Gaps 5;

QY 7 QEKLSPLGEEMRDRARAH-----VDALRTHLAPYSDELR-----QRLAARLEALKE 52
Db 4 QIRMSP--SELRDRAKTYGQSGRDIEDILSRLSQLQDLRSEWEGQAFMRFDQFEQLK- 60

QY 53 NGGARLAEYHAKATEHLSTLSEKAKPALEDLRQGL 87
Db 61 ---PKVTEF-ANLMDQINDQLEKTANAVEEHQQQL 91

RESULT 10
AI3243
transcriptional repressor tram [imported] - Agrobacterium tumefaciens (strain C58, Dupon C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI3243
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyaivin, T.; Levy, R.; Li, M.; McClel ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI3243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <KUR>
A;Cross-references: UNIPROT:Q44452; GB:AE008690; PIDN:AAL46367.1; PID:g17744157; GSPDB: A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: tram
A;Genome: plasmid

Query Match 10.7%; Score 59.5; DB 2; Length 102;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 11:47:05 ; Search time 186 Seconds
(without alignments)
346.462 Million cell updates/sec

Title: US-09-803-918A-2_COPY_156_267
Perfect score: 556
Sequence: 1 QKLHELQEKLSPLGEMRDR.....SFKVSFLSALEEYTKKLNTQ 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 350892

Minimum DB seq length: 0
Maximum DB seq length: 112

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt.02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|--------------------|
| 1 | 327 | 58.8 | 67 | 2 | Q9Y355 | Q9Y355 homo sapien |
| 2 | 246 | 44.2 | 50 | 2 | Q8TDB0 | Q8tdb0 homo sapien |
| 3 | 109.5 | 19.7 | 102 | 2 | Q98TJ9 | Q98tj9 platichthys |
| 4 | 97 | 17.4 | 107 | 1 | APE_SAISC | Q28995 saimiri sci |
| 5 | 93 | 16.7 | 107 | 1 | APE_MACMU | Q28502 macaca mula |
| 6 | 82 | 14.7 | 96 | 2 | Q7P280 | Q7p280 fusobacteri |
| 7 | 79 | 14.2 | 96 | 2 | Q8RH51 | Q8rh51 chromobacte |
| 8 | 78.5 | 14.1 | 110 | 2 | Q7NRA9 | Q7nra9 chromobacte |
| 9 | 77 | 13.8 | 66 | 2 | Q9DFQ4 | Q9dfq4 gillichthys |
| 10 | 76.5 | 13.8 | 96 | 2 | Q9TS51 | Q9ts51 sus scrofa |
| 11 | 72.5 | 13.0 | 104 | 2 | Q72J66 | Q72j66 thermus the |
| 12 | 72.5 | 13.0 | 104 | 2 | AAS81257 | Aas81257 thermus t |
| 13 | 70 | 12.6 | 102 | 2 | Q29258 | Q29258 sus scrofa |
| 14 | 68 | 12.2 | 85 | 2 | Q7Q1M4 | Q7qlm4 anopheles g |
| 15 | 67.5 | 12.1 | 79 | 2 | Q6LD50 | Q6ld50 mus sp. apo |
| 16 | 67.5 | 12.1 | 79 | 2 | AAB35539 | Aab35539 mus sp. a |
| 17 | 67 | 12.1 | 71 | 1 | ST1B_XENLA | Q09005 xenopus lae |
| 18 | 66.5 | 12.0 | 104 | 1 | SL1B_RAT | P09916 rattus norv |
| 19 | 66.5 | 12.0 | 105 | 2 | Q8ZYI9 | Q8zyi9 pyrobaculum |
| 20 | 66 | 11.9 | 84 | 2 | Q82YM0 | Q82ym0 enterococcu |
| 21 | 65 | 11.7 | 84 | 2 | Q7U6M0 | Q7u6m0 synechococc |
| 22 | 64.5 | 11.6 | 98 | 2 | P91785 | P91785 onchocerca |
| 23 | 64 | 11.5 | 88 | 2 | Q9A5D7 | Q9a5d7 caulobacter |
| 24 | 62.5 | 11.2 | 109 | 1 | IATP_BOVIN | P01096 bos taurus |
| 25 | 62 | 11.2 | 97 | 2 | Q9SCK2 | Q9eck2 arabidopsis |
| 26 | 62 | 11.2 | 107 | 2 | P74485 | P74485 synechocyst |
| 27 | 61.5 | 11.1 | 76 | 2 | Q8FRA8 | Q8fra8 corynebacte |
| 28 | 61 | 11.0 | 101 | 2 | Q6Y7N2 | Q6y7n2 staphylococ |
| 29 | 61 | 11.0 | 101 | 2 | AAO47534 | Aao47534 staphyloc |
| 30 | 61 | 11.0 | 104 | 2 | Q8UFZ0 | Q8ufz0 agrobacteri |
| 31 | 61 | 11.0 | 109 | 2 | Q84GY9 | Q84gy9 photorhabdu |

| | | | | | | |
|----|------|------|-----|---|-------------|--------------------|
| 32 | 60.5 | 10.9 | 83 | 2 | Q711L8 | Q711l8 fasciola he |
| 33 | 60.5 | 10.9 | 83 | 2 | CAC86373 | Cac86373 fasciola |
| 34 | 60.5 | 10.9 | 86 | 2 | Q8P6R7 | Q8p6r7 xanthomonas |
| 35 | 60.5 | 10.9 | 89 | 2 | Q8LQ79 | Q8lq79 oryza sativ |
| 36 | 60.5 | 10.9 | 104 | 2 | Q8R814 | Q8r814 thermoanaer |
| 37 | 60 | 10.8 | 85 | 2 | Q9QJL5 | Q9qjl5 human immun |
| 38 | 59.5 | 10.7 | 88 | 1 | APC1_TUPGL | Q9xsns tupaia glis |
| 39 | 59.5 | 10.7 | 97 | 2 | Q92FQ4 | Q92fq4 listeria in |
| 40 | 59.5 | 10.7 | 102 | 1 | TRAM_AGR T5 | Q44452 agrobacteri |
| 41 | 59.5 | 10.7 | 102 | 2 | Q9R6E6 | Q9r6e6 agrobacteri |
| 42 | 59.5 | 10.7 | 107 | 2 | O35693 | O35693 mus musculu |
| 43 | 59.5 | 10.7 | 110 | 2 | Q6PRF2 | Q6prf2 helicobacte |
| 44 | 59.5 | 10.7 | 110 | 2 | Q8KKD9 | Q8kkd9 helicobacte |
| 45 | 59.5 | 10.7 | 110 | 2 | AAS93839 | Aas93839 helicobac |

ALIGNMENTS

RESULT 1

| | | | | | | |
|--------|---|---|------|----|-----|--|
| Q9Y355 | | | | | | |
| ID | Q9Y355 | PRELIMINARY; | PRT; | 67 | AA. | |
| AC | Q9Y355; | | | | | |
| DT | 01-NOV-1999 | (TrEMBLrel. 12, Created) | | | | |
| DT | 01-NOV-1999 | (TrEMBLrel. 12, Last sequence update) | | | | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last annotation update) | | | | |
| DE | Apolipoprotein A1 (Fragment). | | | | | |
| OS | Homo sapiens (Human). | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | | |
| OX | NCBI_TaxID=9606; | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=99216322; PubMed=10198255; | | | | | |
| RA | Hamidi Asl K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.; | | | | | |
| RT | "A novel apolipoprotein A-1 variant, Arg173Pro, associated with | | | | | |
| RT | cardiac and cutaneous amyloidosis."; | | | | | |
| RL | Biochem. Biophys. Res. Commun. 257:584-588(1999). | | | | | |
| DR | EMBL; AF148963; AAD34604.1; -. | | | | | |
| DR | GO; GO:0005576; C:extracellular; IEA. | | | | | |
| DR | GO; GO:0008289; F:lipid binding; IEA. | | | | | |
| DR | GO; GO:0006869; P:lipid transport; IEA. | | | | | |
| DR | GO; GO:0042157; P:lipoprotein metabolism; IEA. | | | | | |
| DR | InterPro; IPR000074; Apolipoprotein. | | | | | |
| DR | InterPro; IPR009074; Apolipo_A_E C3. | | | | | |
| DR | Pfam; PF01442; Apolipoprotein; 1. | | | | | |
| KW | Lipoprotein. | | | | | |
| FT | NON_TER 1 | | | | | |
| FT | NON_TER 67 | | | | | |
| SQ | SEQUENCE 67 AA; 7433 MW; 525E1FEB7BDD5AFB CRC64; | | | | | |

Query Match 58.8%; Score 327; DB 2; Length 67;
Best Local Similarity 98.5%; Pred. No. 2e-19;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|----|--|----|
| Qy | 10 | LSPLGEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARLAEYHAKATEHL | 69 |
| Db | 1 | LSPLGEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARLAEYHAKATEHL | 60 |
| Qy | 70 | STLSEKA 76 | |
| Db | 61 | STLSEKA 67 | |

RESULT 2

| | | | | | | |
|--------|--|---|------|----|-----|--|
| Q8TDB0 | | | | | | |
| ID | Q8TDB0 | PRELIMINARY; | PRT; | 50 | AA. | |
| AC | Q8TDB0; | | | | | |
| DT | 01-JUN-2002 | (TrEMBLrel. 21, Created) | | | | |
| DT | 01-JUN-2002 | (TrEMBLrel. 21, Last sequence update) | | | | |
| DT | 01-OCT-2003 | (TrEMBLrel. 25, Last annotation update) | | | | |
| DE | Apolipoprotein A-1 A175P variant (Fragment). | | | | | |
| OS | Homo sapiens (Human). | | | | | |

| | | | |
|--|---|--|--------------|
| QY | 2 | KLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEALKENGARLAEY | 61 |
| Db | 10 | KAEELVGAVTDKAKELKDETVAKAEELKDKTVEKAEELKNKVVDKAKELKEGAEGKASEL | 69 |
| QY | 62 | HAKATEHLSTLSEKAKPALEDL | 83 |
| Db | 70 | KDKAEKAEELKDKITDGADSL | 91 |
| RESULT 8 | | | |
| Q7NRA9 | Q7NRA9 | PRELIMINARY; | PRT; 110 AA. |
| AC | Q7NRA9; | | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Created) | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last sequence update) | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last annotation update) | |
| DE | Hypothetical protein. | | |
| GN | OrderedLocusNames=CV3874; | | |
| OS | Chromobacterium violaceum. | | |
| OC | Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; | | |
| OC | Neisseriaceae; Chromobacterium. | | |
| OX | NCBI_TaxID=536; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=ATCC 12472 / DSM 30191; | | |
| RX | MEDLINE=22882880; PubMed=14500782; | | |
| RA | Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T., | | |
| RA | Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R., | | |
| RA | Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F., | | |
| RA | Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M., | | |
| RA | Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S., | | |
| RA | Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A., | | |
| RA | Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M., | | |
| RA | Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O., | | |
| RA | Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L., | | |
| RA | Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A., | | |
| RA | Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R., | | |
| RA | Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B., | | |
| RA | Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J., | | |
| RA | Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P., | | |
| RA | Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S., | | |
| RA | di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M., | | |
| RA | Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C., | | |
| RA | Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O., | | |
| RA | Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P., | | |
| RA | Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E., | | |
| RA | Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N., | | |
| RA | Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C., | | |
| RA | Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L., | | |
| RA | Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T., | | |
| RA | Vettore A., Wassem R., Zaha A., Simpson A.J.G.; | | |
| RT | "The complete genome sequence of Chromobacterium violaceum reveals | | |
| RT | remarkable and exploitable bacterial adaptability."; | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003). | | |
| DR | EMBL; AE016923; AAQ61536.1; -- | | |
| KW | Complete proteome; Hypothetical protein. | | |
| SQ | SEQUENCE 110 AA; 12757 MW; 6B6CC3929C615493 CRC64; | | |
| Query Match 14.1%; Score 78.5; DB 2; Length 110; | | | |
| Best Local Similarity 32.6%; Pred. No. 59; | | | |
| Matches 31; Conservative 12; Mismatches 31; Indels 21; Gaps 4; | | | |
| QY | 3 | LHELQEKLSPLGEE-----MRDRAR-----AHVDALRTHLA-----PYSDELQR | 42 |
| Db | 10 | LAELIEQLEPLTRELLEANLRDRPFSSLYGRSEAHVQQLKLTLEQGRDQLSDEQREA | 69 |
| QY | 43 | LAARLEALKENGARLAEYHAKATEHLSTLSEKAK | 77 |
| Db | 70 | L-HRVLIVREETQRQLANWAGQVKDELRLTSLKSSK | 103 |
| RESULT 9 | | | |

| | | | | |
|---|--|--|-----------|-------------------------|
| Q9DFQ4 | Q9DFQ4 | PRELIMINARY; | PRT; | 66 AA. |
| AC | Q9DFQ4; | | | |
| DT | 01-MAR-2001 | (TrEMBLrel. 16, Created) | | |
| DT | 01-MAR-2001 | (TrEMBLrel. 16, Last sequence update) | | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last annotation update) | | |
| DE | Apolipoprotein A-1 (Fragment). | | | |
| OS | Gillichthys seta (Shortjaw mudsucker). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; | | | |
| OC | Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidae; | | | |
| OC | Gobiidae; Gillichthys. | | | |
| OX | NCBI_TaxID=79683; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Liver; | | | |
| RX | MEDLINE=21117151; PubMed=11172064; | | | |
| RA | Gracey A.Y., Troll J.V., Somero G.N.; | | | |
| RT | "Hypoxia-induced gene expression profiling in the euryoxic fish | | | |
| RT | Gillichthys mirabilis."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001). | | | |
| DR | EMBL; AF266178; AAG13298.1; -- | | | |
| DR | GO; GO:0005576; C:extracellular; IEA. | | | |
| DR | GO; GO:0008289; F:lipid binding; IEA. | | | |
| DR | GO; GO:0006869; P:lipid transport; IEA. | | | |
| DR | GO; GO:0042157; P:lipoprotein metabolism; IEA. | | | |
| DR | InterPro; IPR000074; Apolipoprotein. | | | |
| DR | InterPro; IPR009074; Apolipo_A_E_C3. | | | |
| DR | Pfam; PF01442; Apolipoprotein; 1. | | | |
| KW | Lipoprotein. | | | |
| FT | NON_TER | 1 | 1 | |
| FT | NON_TER | 66 | 66 | |
| SQ | SEQUENCE | 66 AA; | 7637 MW; | 0B5B673FA8C91B7D CRC64; |
| Query Match 13.8%; Score 77; DB 2; Length 66; | | | | |
| Best Local Similarity 33.3%; Pred. No. 47; | | | | |
| Matches 14; Conservative 13; Mismatches 15; Indels 0; Gaps 0; | | | | |
| QY | 9 | KLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQRLAARLEAL 50 | | |
| Db | 15 | KLEPIMEEMRAKIEVNVETKSKLVPIDTVREKITERVKAV 56 | | |
| RESULT 10 | | | | |
| Q9TS51 | Q9TS51 | PRELIMINARY; | PRT; | 96 AA. |
| ID | Q9TS51 | | | |
| AC | Q9TS51; | | | |
| DT | 01-MAY-2000 | (TrEMBLrel. 13, Created) | | |
| DT | 01-MAY-2000 | (TrEMBLrel. 13, Last sequence update) | | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last annotation update) | | |
| DE | Myosin heavy chain (Fragment). | | | |
| OS | Sus scrofa (pig). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. | | | |
| OX | NCBI_TaxID=9823; | | | |
| RN | [1] | | | |
| RP | SEQUENCE. | | | |
| RX | MEDLINE=95246271; PubMed=7537184; | | | |
| RA | Inomata T., Hanawa H., Miyanishi T., Yajima E., Nakayama S., Maita T., | | | |
| RA | Kodama M., Izumi T., Shibata A., Abo T.; | | | |
| RT | "Localization of porcine cardiac myosin epitopes that induce | | | |
| RT | experimental autoimmune myocarditis."; | | | |
| RL | Circ. Res. 76:726-733(1995). | | | |
| DR | InterPro; IPR002928; Myosin tail. | | | |
| DR | Pfam; PF01576; Myosin_tail_1; 1. | | | |
| SQ | SEQUENCE | 96 AA; | 11137 MW; | 69943C386226BEEC CRC64; |
| Query Match 13.8%; Score 76.5; DB 2; Length 96; | | | | |
| Best Local Similarity 37.9%; Pred. No. 75; | | | | |
| Matches 22; Conservative 11; Mismatches 16; Indels 9; Gaps 2; | | | | |
| QY | 1 | QKLHELQEKLSPLGEEMRDR--ARAHVDALRTHLAPYSDELQRQRLAARLEALKENGGA 56 | | |
| Db | 1 | QKLHELQEKLSPLGEEMRDR--ARAHVDALRTHLAPYSDELQRQRLAARLEALKENGGA 56 | | |

| | | | |
|--|---|--|----|
| Db | 39 | KKLKELQARIEEBELEAERTARAKVEKLRSDL\$RELEEISER-----LEEAGGA | 89 |
| RESULT 11 | | | |
| Q72J66 | ID | Q72J66 PRELIMINARY; PRT; 104 AA. | |
| AC | Q72J66 | | |
| DT | 05-JUL-2004 | (TrEMBLrel. 27, Created) | |
| DT | 05-JUL-2004 | (TrEMBLrel. 27, Last sequence update) | |
| DT | 05-JUL-2004 | (TrEMBLrel. 27, Last annotation update) | |
| DE | V-type ATPase subunit. | | |
| GN | OrderedLocusNames=TT0913; | | |
| OS | Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039). | | |
| OC | Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; | | |
| OC | Thermus. | | |
| OX | NCBI_TaxID=262724; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | PubMed=15064768; | | |
| RA | Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T., | | |
| RA | Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., | | |
| RA | Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., | | |
| RA | Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; | | |
| RT | "The genome sequence of the extreme thermophile Thermus | | |
| RT | thermophilus."; | | |
| RL | Nat. Biotechnol. 22:547-553(2004). | | |
| DR | EMBL; AE017304; AAS81257.1; -. | | |
| KW | Complete proteome. | | |
| SQ | SEQUENCE 104 AA; 11672 MW; A01FBCE249900B1F CRC64; | | |
| Query Match 13.0%; Score 72.5; DB 2; Length 104; | | | |
| Best Local Similarity 37.9%; Pred. No. 1.7e+02; | | | |
| Matches 22; Conservative 8; Mismatches 21; Indels 7; Gaps 2; | | | |
| QY | 3 | LHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGGARLAE | 60 |
| : : : : : : : : : : : : : : : | | | |
| Db | 43 | LEEAEAKAKALEAQYRERERAETEAL---LARY----RERAEAEAKAVREKAMARLDE | 93 |
| RESULT 12 | | | |
| AAS81257 | ID | AAS81257 PRELIMINARY; PRT; 104 AA. | |
| AC | AAS81257 | | |
| DT | 14-APR-2004 | (TrEMBLrel. 27, Created) | |
| DT | 14-APR-2004 | (TrEMBLrel. 27, Last sequence update) | |
| DT | 11-MAY-2004 | (TrEMBLrel. 27, Last annotation update) | |
| DE | V-type ATPase subunit. | | |
| GN | TT0913. | | |
| OS | Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039). | | |
| OC | Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; | | |
| OC | Thermus. | | |
| OX | NCBI_TaxID=262724; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | PubMed=15064768; | | |
| RA | Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T., | | |
| RA | Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., | | |
| RA | Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., | | |
| RA | Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; | | |
| RT | "The genome sequence of the extreme thermophile Thermus | | |
| RT | thermophilus."; | | |
| RL | Nat. Biotechnol. 22:547-553(2004). | | |
| DR | EMBL; AE017304; AAS81257.1; -. | | |
| SQ | SEQUENCE 104 AA; 11672 MW; A01FBCE249900B1F CRC64; | | |
| Query Match 13.0%; Score 72.5; DB 2; Length 104; | | | |
| Best Local Similarity 37.9%; Pred. No. 1.7e+02; | | | |
| Matches 22; Conservative 8; Mismatches 21; Indels 7; Gaps 2; | | | |
| QY | 3 | LHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGGARLAE | 60 |
| : : : : : : : : : : : : : : : | | | |
| Db | 43 | LEEAEAKAKALEAQYRERERAETEAL---LARY----RERAEAEAKAVREKAMARLDE | 93 |

| | | | |
|---|--|---|-----|
| RESULT 13 | | | |
| Q29258 | ID | Q29258 PRELIMINARY; PRT; 102 AA. | |
| AC | Q29258 | | |
| DT | 01-NOV-1996 | (TrEMBLrel. 01, Created) | |
| DT | 01-NOV-1996 | (TrEMBLrel. 01, Last sequence update) | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last annotation update) | |
| DE | Apolipoprotein A-IV (Fragment). | | |
| OS | Sus scrofa (Pig). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. | | |
| OX | NCBI_TaxID=9823; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=Small intestine; | | |
| RX | MEDLINE=96327607; PubMed=8672129; | | |
| RA | Winteroe A.K., Fredholm M., Davies W.; | | |
| RT | "Evaluation and characterization of a porcine small intestine cDNA | | |
| RT | library."; | | |
| RL | Mamm. Genome 7:509-517(1996). | | |
| DR | EMBL; F14546; CAA23119.1; -. | | |
| DR | GO; GO:0005576; C:extracellular; IEA. | | |
| DR | GO; GO:0008289; F:lipid binding; IEA. | | |
| DR | GO; GO:0006869; P:lipid transport; IEA. | | |
| DR | GO; GO:0042157; P:lipoprotein metabolism; IEA. | | |
| DR | InterPro; IPR000074; Apolipoprotein. | | |
| DR | InterPro; IPR009074; Apolipo_A_E_C3. | | |
| DR | Pfam; PF01442; Apolipoprotein; 1. | | |
| KW | Lipoprotein. | | |
| FT | NON TER 102 102 | | |
| SQ | SEQUENCE 102 AA; 11534 MW; 123EAEAL34FBC8A CRC64; | | |
| Query Match 12.6%; Score 70; DB 2; Length 102; | | | |
| Best Local Similarity 31.2%; Pred. No. 2.7e+02; | | | |
| Matches 15; Conservative 11; Mismatches 22; Indels 0; Gaps 0; | | | |
| QY | 5 | ELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKE | 52 |
| : : : : : : : : : : : : | | | |
| Db | 53 | ELTQQLNTLFDKLGEVNTYTEDLQXKLVFPFATELHERLTCKDXEKLE | 100 |
| RESULT 14 | | | |
| Q7Q1M4 | ID | Q7Q1M4 PRELIMINARY; PRT; 85 AA. | |
| AC | Q7Q1M4 | | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Created) | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last sequence update) | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last annotation update) | |
| DE | AgCP8687 (Fragment). | | |
| GN | Name=agCG49971; ORFNames=ENSANGG000000007463; | | |
| OS | Anopheles gambiae str. PEST. | | |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; | | |
| OC | Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles. | | |
| OX | NCBI_TaxID=180454; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=PEST; | | |
| RA | Anopheles Genome Sequencing Consortium; | | |
| RL | Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. | | |
| CC | -!- CAUTION: The sequence shown here is derived from an | | |
| CC | EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is | | |
| CC | preliminary data. | | |
| DR | EMBL; AAB01008980; EAA14425.1; -. | | |
| FT | NON TER 1 1 | | |
| SQ | SEQUENCE 85 AA; 9772 MW; 769097995041FB44 CRC64; | | |
| Query Match 12.2%; Score 68; DB 2; Length 85; | | | |
| Best Local Similarity 28.3%; Pred. No. 3.3e+02; | | | |
| Matches 17; Conservative 18; Mismatches 21; Indels 4; Gaps 1; | | | |
| QY | 37 | DELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKV | 96 |
| : : : : : : : : : : : : : : : : | | | |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 11:55:03 ; Search time 152 Seconds
(without alignments)
264.327 Million cell updates/sec

Title: US-09-803-918A-2_COPY_156_267
Perfect score: 556
Sequence: 1 QKLHELQEKLSPLGEMRDR.....SPKVSFLSALEEYTKLNTQ 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1169828

Minimum DB seq length: 0
Maximum DB seq length: 112

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|--------------------|
| 1 | 244 | 43.9 | 49 | 6 | ABR44037 Human Apo |
| 2 | 244 | 43.9 | 49 | 6 | ABR44039 Human Apo |
| 3 | 244 | 43.9 | 49 | 6 | ABR44038 Human Apo |
| 4 | 240 | 43.2 | 49 | 6 | ABR44040 Baboon Ap |
| 5 | 186 | 33.5 | 49 | 6 | ABR44041 Rabbit Ap |
| 6 | 161 | 29.0 | 33 | 7 | ADC29656 Antioxida |
| 7 | 157.5 | 28.3 | 48 | 6 | ABR44042 Pig ApoA- |
| 8 | 153 | 27.5 | 33 | 7 | ADC29655 Antioxida |
| 9 | 129 | 23.2 | 49 | 6 | ABR44044 Chicken A |
| 10 | 113 | 20.3 | 47 | 6 | ABR44043 Rat ApoA- |
| 11 | 111 | 20.0 | 85 | 8 | ADP87442 Human apo |
| 12 | 100 | 18.0 | 38 | 4 | AAO08726 Human pol |
| 13 | 100 | 18.0 | 85 | 8 | ADP87441 Monkey ap |
| 14 | 99 | 17.8 | 85 | 8 | ADP87439 Pig apoli |
| 15 | 96 | 17.3 | 85 | 8 | ADP87440 Baboon ap |
| 16 | 94 | 16.9 | 18 | 7 | ADC29635 Antioxida |
| 17 | 91 | 16.4 | 22 | 4 | AAG62608 Apolipopr |
| 18 | 90 | 16.2 | 18 | 7 | ADC29638 Antioxida |
| 19 | 90 | 16.2 | 96 | 8 | ADP87420 Squirrel |
| 20 | 87 | 15.6 | 18 | 7 | ADC29642 Antioxida |
| 21 | 87 | 15.6 | 96 | 8 | ADP87422 Baboon ap |
| 22 | 87 | 15.6 | 96 | 8 | ADP87423 Rhesus ma |
| 23 | 87 | 15.6 | 96 | 8 | ADP87421 Monkey ap |
| 24 | 86 | 15.5 | 18 | 7 | ADC29636 Antioxida |
| 25 | 86 | 15.5 | 18 | 7 | ADC29639 Antioxida |

| | | | | | | |
|----|------|------|-----|---|----------|--------------------|
| 26 | 86 | 15.5 | 18 | 7 | ADC29634 | Adc29634 Antioxida |
| 27 | 85 | 15.3 | 18 | 7 | ADC29637 | Adc29637 Antioxida |
| 28 | 84.5 | 15.2 | 96 | 8 | ADP87430 | Adp87430 Gorilla a |
| 29 | 84 | 15.1 | 18 | 7 | ADC29627 | Adc29627 Antioxida |
| 30 | 83 | 14.9 | 18 | 7 | ADC29640 | Adc29640 Antioxida |
| 31 | 83 | 14.9 | 18 | 7 | ADC29651 | Adc29651 Antioxida |
| 32 | 82 | 14.7 | 17 | 2 | AAR98474 | Aar98474 Anti-arte |
| 33 | 82 | 14.7 | 18 | 7 | ADC29649 | Adc29649 Antioxida |
| 34 | 82 | 14.7 | 18 | 7 | ADC29646 | Adc29646 Antioxida |
| 35 | 82 | 14.7 | 18 | 7 | ADC29644 | Adc29644 Antioxida |
| 36 | 82 | 14.7 | 18 | 7 | ADC29647 | Adc29647 Antioxida |
| 37 | 82 | 14.7 | 18 | 7 | ADC29650 | Adc29650 Antioxida |
| 38 | 81 | 14.6 | 17 | 6 | ABR44036 | Abr44036 Human Apo |
| 39 | 81 | 14.6 | 17 | 6 | ABR44035 | Abr44035 Human Apo |
| 40 | 81 | 14.6 | 96 | 8 | ADP87428 | Adp87428 Orangutan |
| 41 | 81 | 14.6 | 96 | 8 | ADP87429 | Adp87429 Chimpanze |
| 42 | 81 | 14.6 | 110 | 2 | AAR12387 | Aar12387 Amplified |
| 43 | 80.5 | 14.5 | 107 | 8 | ADP87437 | Adp87437 Mouse apo |
| 44 | 80.5 | 14.5 | 107 | 8 | ADP87436 | Adp87436 Mouse apo |
| 45 | 80.5 | 14.5 | 107 | 8 | ADP87434 | Adp87434 Mouse apo |

ALIGNMENTS

RESULT 1
ABR44037
ID ABR44037 standard; peptide; 49 AA.
XX

AC ABR44037;

DT 04-AUG-2003 (first entry)

XX Human ApoA-I protein fragment.

DE Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; human;
KW cardiovascular disorder.
XX

OS Homo sapiens.

XX WO2003035691-A1.

PD 01-MAY-2003.

XX 25-OCT-2002; 2002WO-CA001615.

XX 26-OCT-2001; 2001US-0335075P.

XX (XENO-) XENON GENETICS INC.
(UYBR-) UNIV BRITISH COLUMBIA.

PI Brownlie AJ, Dube M, Samuels M, Hayden MR;

XX WPI; 2003-449258/42.

XX New Apolipoprotein A-1 mutation, useful for preparing a composition for
treating cardiovascular disorder.

PS Disclosure; Fig 4; 52pp; English.

XX The invention relates to a mutation of the apolipoprotein A-I (ApoA-I)
comprising a leucine to proline variant in position 178. The mutant ApoA-
I polynucleotide is useful for preparing a composition for treating
cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments
from various species where the leucine at position 178 is highly
conserved except in pig (ABR44042)

SQ Sequence 49 AA;

Query Match 43.9%; Score 244; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polynucleotide is useful for preparing a composition for treating cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments from various species where the leucine at position 178 is highly conserved except in pig (ABR44042)

XX

SQ Sequence 49 AA;

Query Match 43.2%; Score 240; DB 6; Length 49;
Best Local Similarity 98.0%; Pred. No. 4.8e-17;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 26 DALRTHLAPYSDELQRLLAARLEALKENGARLAAYHAKATEHLSLSE 74
|||||
Db 1 DALRTHLAPYSDELQRLLAARLEALKENGARLAAYHAKASEHLSLSE 49

RESULT 5
ABR44041
ID ABR44041 standard; peptide; 49 AA.
XX
AC ABR44041;
XX
DT 04-AUG-2003 (first entry)
XX
DE Rabbit ApoA-I protein fragment.
XX
KW Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; rabbit;
KW cardiovascular disorder.
XX
OS Oryctolagus cuniculus.
XX
PN WO2003035691-A1.
XX
PD 01-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-CA001615.
XX
PR 26-OCT-2001; 2001US-0335075P.
XX
PA (XENO-) XENON GENETICS INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Brownlie AJ, Dube M, Samuels M, Hayden MR;
XX
DR WPI; 2003-449258/42.
XX
PT New Apolipoprotein A-1 mutation, useful for preparing a composition for treating cardiovascular disorder.
XX
PS Disclosure; Fig 4; 52pp; English.
XX

CC The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polynucleotide is useful for preparing a composition for treating cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments from various species where the leucine at position 178 is highly conserved except in pig (ABR44042)

XX

SQ Sequence 49 AA;

Query Match 33.5%; Score 186; DB 6; Length 49;
Best Local Similarity 77.6%; Pred. No. 1.5e-11;
Matches 38; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 26 DALRTHLAPYSDELQRLLAARLEALKENGARLAAYHAKATEHLSLSE 74
|||||
Db 1 DTLRTKLAPYSNELQORLAARLESIKEGGASLAAYQAKAREHLSVLSE 49

RESULT 6
ADC29656

ID ADC29656 standard; peptide; 33 AA.
XX
AC ADC29656;
XX
DT 18-DEC-2003 (first entry)
XX
DE Antioxidant peptide #31.
XX
KW antioxidant; cardiovascular disease; ischaemia; bone disease;
KW inflammatory related disease; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003087819-A1.
XX
PD 08-MAY-2003.
XX
PF 08-MAY-2002; 2002US-00142238.
XX
PR 09-MAY-2001; 2001US-0289944P.
XX
PA (BIEL/) BIELICKI J K.
XX
PI Bielicki JK;
XX
DR WPI; 2003-786946/74.
XX
PT New cysteine-containing peptides, having antioxidant properties, useful for diagnosing and treating cardiovascular disease, ischemia, bone disease and other inflammatory related diseases.
PT
XX
PS Example 8; SEQ ID NO 31; 49pp; English.
XX
CC The invention relates to an antioxidant peptide. The methods and compositions of the present invention are useful for diagnosing and treating cardiovascular disease, ischaemia, bone disease and other inflammatory related diseases. The present sequence represents the amino acid sequence of a peptide with antioxidant activity.
XX
SQ Sequence 33 AA;

Query Match 29.0%; Score 161; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 PALEDLRQGLLPVLESFKVSFLSALEYTKKLN 110
|||||
Db 1 PALEDLRQGLLPVLESFKVSFLSALEYTKKLN 33

RESULT 7
ABR44042
ID ABR44042 standard; peptide; 48 AA.
XX
AC ABR44042;
XX
DT 04-AUG-2003 (first entry)
XX
DE Pig ApoA-I protein fragment.
XX
KW Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; pig;
KW cardiovascular disorder.
XX
OS Sus sp.
XX
PN WO2003035691-A1.
XX
PD 01-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-CA001615.
XX
PR 26-OCT-2001; 2001US-0335075P.

XX Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; rat;
KW cardiovascular disorder.
XX
OS Rattus sp.
XX
PN WO2003035691-A1.
XX
PD
XX
XX
PF 25-OCT-2002; 2002WO-CA001615.
XX
PR 26-OCT-2001; 2001US-0335075P.
XX
XX (XENO-) XENON GENETICS INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Brownlie AJ, Dube M, Samuels M, Hayden MR;
XX
DR WPI; 2003-449258/42.
XX
PT New Apolipoprotein A-1 mutation, useful for preparing a composition for
PT treating cardiovascular disorder.
XX
PS Disclosure; Fig 4; 52pp; English.
XX
CC The invention relates to a mutation of the apolipoprotein A-I (ApoA-I)
CC comprising a leucine to proline variant in position 178. The mutant ApoA-
CC I polynucleotide is useful for preparing a composition for treating
CC cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments
CC from various species where the leucine at position 178 is highly
CC conserved except in pig (ABR44042)
XX
SQ Sequence 47 AA;

Query Match 20.3%; Score 113; DB 6; Length 47;
Best Local Similarity 49.0%; Pred. No. 0.00041;
Matches 24; Conservative 7; Mismatches 16; Indels 2; Gaps 1;

QY 26 DALRTHLAPYSDELQRRLAARLEALKENGARLAEVHAKATEHLSTLSE 74
Db 1 DALRAKFGLYSDQMRENLAQRLTEIKNH--PTLIEYHTKASDHLKLTGE 47

RESULT 11
ADP87442
ID ADP87442 standard; protein; 85 AA.
XX
AC ADP87442;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human apolipoprotein A (APO-A) precursor protein.
XX
KW Browsable database system; ontology; protein analysis;
KW gene product classification; genomic analysis; apolipoprotein A; APO-A;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004053769-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US038935.
XX
PR 09-DEC-2002; 2002US-0431879P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;
PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;
PI Doremieux O;

XX WPI; 2004-480967/45.
DR
XX Browsable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.
XX
PS Disclosure; SEQ ID NO 49; 113pp; English.
XX
CC The invention relates to a browsable database system for use with
CC biological information, comprises a datastore, an ontology of categories
CC of biological functions, an input receptive, a recognizer and an output.
CC The invention also provides a method of operation for use with a
CC browsable biological database system. The browsable database system and
CC methods are useful in analysing protein sequences, classifying gene
CC products, predicting biological role for pathway building, enhancing
CC interpretation of expression information, providing protein function and
CC in facilitating comparative genomic analysis. The present sequence is
CC human apolipoprotein A (APO-A) IV precursor protein. This sequence is
CC used to illustrate the method of the invention.
XX
SQ Sequence 85 AA;

Query Match 20.0%; Score 111; DB 8; Length 85;
Best Local Similarity 32.5%; Pred. No. 0.0014;
Matches 27; Conservative 16; Mismatches 40; Indels 0; Gaps 0;

QY 5 ELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGARLAHYHAK 64
Db 2 ELTQQLNALFQDKLGEVNTYAGDLQKLVPFATELHERLAKDSEKLKEEIGKELELRAR 61

QY 65 ATEHLSTLSEKAKPALEDLRQGL 87
Db 62 LLPHANEVVSQKIGDNLRELQORL 84

RESULT 12
AAO08726
ID AAO08726 standard; protein; 38 AA.
XX
AC AAO08726;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 22618.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI88657.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX


```

Query Match      17.8%; Score 99; DB 8; Length 85;
Best Local Similarity 28.9%; Pred. NO. 0.023;
Matches 24; Conservative 18; Mismatches 41; Indels 0; Gaps 0;

```

| | | | | | | | |
|----|---|-----------------------|------------------|---------------|----------|-------|----|
| Qy | 5 | ELQEKLSPLGEENRDRARAHV | DALRTHLAPYSDELQR | LAARLEALKENG | GARLA | EYHAK | 64 |
| | | : : : : | : : : : | : : : | : | : | |
| Db | 2 | ELTQQLNTLFODKLGEVNTY | TEDLOKKLVPFATL | HERLTKDSEKKEE | IRRELEEL | RAR | 61 |
| | | : : : : | : : : : | : : : | : | : | |

| | | | |
|----------------|----|--------------------------|----|
| Qy | 65 | ATEHLSTLSEKAKPALEDLRQGL | 87 |
| | | : : : : | |
| D _b | 62 | LLPHATEVSKQIGDNRVRELQORL | 84 |

RESULT 15

ADP87440
ID ADP87440 standard; protein; 85 AA.

AC ADP87440:

DT 09-SEP-2004 (first entry)

DE Baboon apolipoprotein A (APO-A) IV precursor protein.

KW Browsable database system; ontology; protein analysis;

gene product classification; genomic analysis; apolipoprotein A; APO-A; baboon.

OS Papio anubis.

PN WO2004053769-A2.

PD 24-JUN-2004.

PF 09-DEC-2003; 2003WO-US038935.

PR 09-DEC-2002; 2002US-0431879P.

PA (APPL-) APPLERA CORP.

PI Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N;

PI Ladunga I, Lazareva B, Muruganujan A, Rabkin S, Vandergriff J;

PI Doremiex O;

DR WPI; 2004-480967/45.

PT Browsable database system, for e.g. analyzing protein sequences, and
PT predicting a biological role, comprises a datastore, an ontology of
PT categories of biological functions, an input receptive, a recognizer, and
PT an output.

PS Disclosure; SEQ ID NO 47; 113pp; English.

The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is baboon apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.

SQ Sequence 85 AA;

| | | | | |
|-----------------------|------------------|------------------|-----------|------------|
| Query Match | 17.3%; | Score 96; | DB 8; | Length 85; |
| Best Local Similarity | 28.9%; | Pred. No. 0.046; | | |
| Matches 24: | Conservative 18; | Mismatches 41; | Indels 0; | Gaps 0; |

| | | | | | | | | | | | | | | | | | | |
|----|------|--|-----|--|---|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Qy | : : | : | - - | | - | | | | | | | | | | | | | |
| | 5 | ELQEKLSPICEEMDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARGARAEYHAK | 64 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|----|------|--|----|---|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Db | : : | : | - | - | | | | | | | | | | | | | | |
| | 2 | ELTOOLNALFODKLGVEVNTYAGDLQKKLVFPATELHERLAKDSKKLKERTIRKELEEVRAR | 61 | | | | | | | | | | | | | | | |


```
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 33
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(33)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-30

Query Match      27.5%; Score 153; DB 14; Length 33;
Best Local Similarity 97.0%; Pred. No. 8.3e-09;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 78 PALEDLRQGLLPVLESFKVSFLSALEEYTKKLN 110
    |||||
Db 1 PALEDLRQGLLPVLESFCVSFLSALEEYTKKLN 33

RESULT 3
US-10-465-789A-58
; Sequence 58, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 10
US-10-465-789A-58

Query Match      21.0%; Score 117; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 PVLESFKVSFLSALEEYTKKLNQTQ 112
    |||||
Db 1 PVLESFKVSFLSALEEYTKKLNQTQ 24

RESULT 4
US-10-465-789A-54
; Sequence 54, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 6
US-10-465-789A-54

Query Match      20.3%; Score 113; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PLGEEMRDRARAHVDALRTHLA 33
    |||||
Db 1 PLGEEMRDRARAHVDALRTHLA 22

RESULT 5
US-10-465-789A-55
; Sequence 55, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 7
US-10-465-789A-55

Query Match      19.8%; Score 110; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 PYSDELFRQLAARLEALKENG 55
    |||||
Db 1 PYSDELFRQLAARLEALKENG 22

RESULT 6
US-10-465-789A-56
```

; Sequence 56, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilia G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 8
US-10-465-789A-56

Query Match 19.4%; Score 108; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 ARLAEYHAKATEHLSTLSEKAK 77
| | | | | | | | | | | | | | | | | |
Db 1 ARLAEYHAKATEHLSTLSEKAK 22

RESULT 7
US-10-142-238A-10
; Sequence 10, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-10

Query Match 16.9%; Score 94; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GEEMDRARAHVDALRTH 31
| | | | | | | | | | | | | | | | | |
Db 1 GEEMDRARAHVDALRTH 18

RESULT 8
US-10-142-238A-13
; Sequence 13, Application US/10142238A
; Publication No. US20030087819A1

; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-13

Query Match 16.2%; Score 90; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 0.015;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GEEMDRARAHVDALRTH 31
| | | | | | | | | | | | | | | | | |
Db 1 GEEMDRARAHVDALRTH 18

RESULT 9
US-10-142-238A-17
; Sequence 17, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-17

Query Match 15.6%; Score 87; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 PVLESFKVSFLSALEEYT 106
| | | | | | | | | | | | | | | | | |
Db 1 PVLESFKVSFLSALEEYT 18

RESULT 10
US-10-142-238A-9
; Sequence 9, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944

```
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-9
```

```
Query Match      15.5%; Score 86; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 0.038;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      14 GEEMDRARAHVDALRTH 31
      ||||| ||||| ||||| |||||
Db      1 GEEMDCARAHVDALRTH 18
```

```
RESULT 11
US-10-142-238A-11
; Sequence 11, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-11
```

```
Query Match      15.5%; Score 86; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 0.038;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      14 GEEMDRARAHVDALRTH 31
      ||||| ||||| ||||| |||||
Db      1 GEEMCDARAHVDALRTH 18
```

```
RESULT 12
US-10-142-238A-14
; Sequence 14, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
```

```
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-14
```

```
Query Match      15.5%; Score 86; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 0.038;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      14 GEEMDRARAHVDALRTH 31
      ||||| ||||| ||||| |||||
Db      1 GEEMDRACAHVDALRTH 18
```

```
RESULT 13
US-10-142-238A-12
; Sequence 12, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-12
```

```
Query Match      15.3%; Score 85; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 0.048;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      14 GEEMDRARAHVDALRTH 31
      ||||| ||||| ||||| |||||
Db      1 GEEMRCARAHVDALRTH 18
```

```
RESULT 14
US-10-142-238A-2
; Sequence 2, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-2
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Query Match      15.1%; Score 84; DB 14; Length 18;
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Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 SDELRQRLEARLEAKEN 53
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Db 1 SDELRQRLEARLEAKEN 18

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RESULT 15
US-10-142-238A-15
; Sequence 15, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/289,944
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-15

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| Query Match | 14.9%; | Score 83; | DB 14; | Length 18; |
| Best Local Similarity | 94.4%; | Pred. No. 0.078; | | |
| Matches 17; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |

QY **14** GEEMDRARAHVDALRTH 31
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Db **1** GEEMDRARACVDALRTH 18

Search completed: December 21, 2004, 11:46:57
Job time : 60 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2004, 11:46:06 ; Search time 38 Seconds
(without alignments)
195.464 Million cell updates/sec

Title: US-09-803-918A-2_COPY_156_267
Perfect score: 556
Sequence: 1 QKLHELQEKLSPLGEMRDR.....SPKVSFLSALEYTKKLNTQ 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 320001

Minimum DB seq length: 0
Maximum DB seq length: 112

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|---------------------------------------|
| 1 | 86 | 15.5 | 64 | 2 | US-08-292-870-1 Sequence 1, Appli |
| 2 | 80.5 | 14.5 | 110 | 1 | US-07-849-389-7 Sequence 7, Appli |
| 3 | 68.5 | 12.3 | 100 | 4 | US-09-147-875A-2 Sequence 2, Appli |
| 4 | 67.5 | 12.1 | 70 | 6 | 5182364-4 Patent No. 5182364 |
| 5 | 67.5 | 12.1 | 101 | 2 | US-08-710-749-1 Sequence 1, Appli |
| 6 | 66.5 | 12.0 | 100 | 4 | US-09-147-875A-3 Sequence 3, Appli |
| 7 | 66.5 | 12.0 | 101 | 2 | US-08-710-749-2 Sequence 2, Appli |
| 8 | 66.5 | 12.0 | 104 | 3 | US-08-777-708C-5 Sequence 5, Appli |
| 9 | 65 | 11.7 | 69 | 6 | 5168045-4 Patent No. 5168045 |
| 10 | 64.5 | 11.6 | 70 | 6 | 5177189-3 Patent No. 5177189 |
| 11 | 63.5 | 11.4 | 100 | 4 | US-09-147-875A-4 Sequence 4, Appli |
| 12 | 62.5 | 11.2 | 101 | 2 | US-08-710-749-3 Sequence 3, Appli |
| 13 | 62.5 | 11.2 | 109 | 2 | US-08-893-042-4 Sequence 4, Appli |
| 14 | 60.5 | 10.9 | 100 | 4 | US-09-147-875A-5 Sequence 5, Appli |
| 15 | 59.5 | 10.7 | 77 | 1 | US-08-182-175A-57 Sequence 57, Appl |
| 16 | 59.5 | 10.7 | 77 | 1 | US-08-474-633A-75 Sequence 75, Appl |
| 17 | 59.5 | 10.7 | 77 | 4 | US-08-823-771-75 Sequence 75, Appl |
| 18 | 59.5 | 10.7 | 77 | 5 | PCT-US92-06412-57 Sequence 57, Appl |
| 19 | 59.5 | 10.7 | 101 | 2 | US-08-710-749-4 Sequence 4, Appli |
| 20 | 59 | 10.6 | 40 | 3 | US-09-214-742-2 Sequence 2, Appli |
| 21 | 59 | 10.6 | 40 | 3 | US-09-255-331-2 Sequence 2, Appli |
| 22 | 59 | 10.6 | 41 | 3 | US-08-584-043A-76 Sequence 76, Appl |
| 23 | 59 | 10.6 | 70 | 4 | US-09-489-039A-8458 Sequence 8458, Ap |
| 24 | 59 | 10.6 | 94 | 4 | US-09-340-620A-67 Sequence 67, Appl |
| 25 | 59 | 10.6 | 99 | 4 | US-09-147-875A-13 Sequence 13, Appl |
| 26 | 59 | 10.6 | 108 | 2 | US-08-710-749-25 Sequence 25, Appl |
| 27 | 59 | 10.6 | 108 | 4 | US-09-147-875A-26 Sequence 26, Appl |

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| 28 | 58.5 | 10.5 | 107 | 1 | US-08-182-175A-105 Sequence 105, App |
| 29 | 58.5 | 10.5 | 107 | 1 | US-08-474-633A-92 Sequence 92, Appl |
| 30 | 58.5 | 10.5 | 107 | 4 | US-08-823-771-92 Sequence 92, Appl |
| 31 | 58.5 | 10.5 | 107 | 5 | PCT-US92-06412-105 Sequence 105, App |
| 32 | 58 | 10.4 | 101 | 2 | US-08-710-749-5 Sequence 5, Appli |
| 33 | 57.5 | 10.3 | 100 | 4 | US-09-147-875A-12 Sequence 12, Appl |
| 34 | 57.5 | 10.3 | 103 | 4 | US-09-513-999C-8123 Sequence 8123, Ap |
| 35 | 57.5 | 10.3 | 106 | 4 | US-09-252-991A-24884 Sequence 24884, A |
| 36 | 57 | 10.3 | 96 | 4 | US-09-583-110-3341 Sequence 3341, Ap |
| 37 | 57 | 10.3 | 105 | 4 | US-09-071-035-292 Sequence 292, App |
| 38 | 57 | 10.3 | 110 | 4 | US-09-270-767-58246 Sequence 58246, A |
| 39 | 56.5 | 10.2 | 98 | 4 | US-09-147-875A-1 Sequence 1, Appli |
| 40 | 56.5 | 10.2 | 100 | 4 | US-09-147-875A-6 Sequence 6, Appli |
| 41 | 56.5 | 10.2 | 103 | 4 | US-09-270-767-34122 Sequence 34122, A |
| 42 | 56.5 | 10.2 | 103 | 4 | US-09-270-767-49339 Sequence 49339, A |
| 43 | 56.5 | 10.2 | 108 | 4 | US-09-270-767-35185 Sequence 35185, A |
| 44 | 56.5 | 10.2 | 108 | 4 | US-09-270-767-50402 Sequence 50402, A |
| 45 | 56 | 10.1 | 103 | 4 | US-09-252-991A-29532 Sequence 29532, A |

ALIGNMENTS

RESULT 1
US-08-292-870-1
; Sequence 1, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-1

Query Match      15.5%; Score 86; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKLHELQEKLSPLGEEM 17
Db 48 QKLHELQEKLSPLGEEM 64

RESULT 2
US-07-849-389-7
; Sequence 7, Application US/07849389
; Patent No. 5525493
; GENERAL INFORMATION:
; APPLICANT: HORNES, Erik
; APPLICANT: UHLEN, Mathias
; TITLE OF INVENTION: CLONING METHOD AND KIT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/849,389
; FILING DATE: 19920519
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16787/168/DFBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-849-389-7

Query Match      14.5%; Score 80.5; DB 1; Length 110;
Best Local Similarity 30.4%; Pred. No. 0.21;
Matches 28; Conservative 13; Mismatches 22; Indels 29; Gaps 3;

QY 5 ELQEKLSPLGEEMDRAR-----AHVDALRTHLAPY-----SDELRQR 42
Db 9 ELEEQLTPVAEETRARLSKELQAAEAPLGADMEDVGRRLVQYRGEVQAMLGQSTEELRVR 68

QY 43 LAARLEALK-----ENGARLAEYHAKATE 67
Db 69 LASHLRKLRKRLRDADDLQKRLAVYQAGARE 100

RESULT 3
US-09-147-875A-2
; Sequence 2, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-2

Query Match      12.3%; Score 68.5; DB 4; Length 100;
Best Local Similarity 26.7%; Pred. No. 3.7;
Matches 23; Conservative 16; Mismatches 34; Indels 13; Gaps 3;

QY 2 KLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARLAEY 61
Db 24 ELDAKQAKLSKL-EELSDK----IDELDAEIA-----KLEKNVEDFKNSNGEQAEQY 70

QY 62 HAKATEHLSTLSEKAKPALEDLRQGL 87
Db 71 RAAAEEDLAAKQAELEKTEADLKKAV 96

RESULT 4
5182364-4
; Patent No. 5182364
; APPLICANT: DYER, CHERYL A.; CURTISS, LINDA K.; SMITH, RICHARD
; TITLE OF INVENTION: POLYPEPTIDE ANALOGS OF APOLIPOPROTEIN E
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,158
; FILING DATE: 26-FEB-1990
; SEQ ID NO:4:
; LENGTH: 70
5182364-4

Query Match      12.1%; Score 67.5; DB 6; Length 70;
Best Local Similarity 27.4%; Pred. No. 3;
Matches 20; Conservative 13; Mismatches 31; Indels 9; Gaps 1;

QY 15 EEMDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARLAEYHAKATEHLSTLSE 74
Db 3 EELRVRLASHLRKLRKRLRDADDLQKRLAVYQST-----EELRVRLASHLRKLRK 53

QY 75 KAKPALEDLRQGL 87
Db 54 RLLEDADDLQKRL 66

RESULT 5
US-08-710-749-1
; Sequence 1, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-1

Query Match 12.1%; Score 67.5; DB 2; Length 101;
Best Local Similarity 27.2%; Pred. No. 4.9;
Matches 22; Conservative 15; Mismatches 31; Indels 13; Gaps 3;

QY 7 QEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLLAARLEALKENGGAARLAAYHAKAT 66
Db 30 QAKLSKL-BELSDK----IDELDAEIA-----KLEKNVEDFKNSNGEQAEQYRAAAE 76

QY 67 EHLSTLSEKAKPALEDLRQGL 87
Db 77 EDLAAKQAELEKTEADLKKAV 97

RESULT 6
US-09-147-875A-3
; Sequence 3, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-3

Query Match 12.0%; Score 66.5; DB 4; Length 100;
Best Local Similarity 26.7%; Pred. No. 6.2;
Matches 23; Conservative 15; Mismatches 35; Indels 13; Gaps 3;

QY 2 KLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLLAARLEALKENGGAARLAAY 61
Db 24 ELDAKQAKLSKL-BELSDK----IDELDAEIA-----KLEKNVEDFKNSNGEAEQY 70

QY 62 HAKATEHLSTLSEKAKPALEDLRQGL 87
Db 71 RAAAGEDLAAKQAELEKTEADLKKAV 96

RESULT 7
US-08-710-749-2
; Sequence 2, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan

; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-2

Query Match 12.0%; Score 66.5; DB 2; Length 101;
Best Local Similarity 27.2%; Pred. No. 6.3;
Matches 22; Conservative 15; Mismatches 31; Indels 13; Gaps 3;

QY 7 QEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLLAARLEALKENGGAARLAAYHAKAT 66
Db 30 QAKLSKL-BELSDK----IDELDAEIA-----KLEKNVEDFKNSNGEQAEQYRAAAG 76

QY 67 EHLSTLSEKAKPALEDLRQGL 87
Db 77 EDLAAKQAELEKTEADLKKAV 97

RESULT 8
US-08-777-708C-5
; Sequence 5, Application US/08777708C
; Patent No. 6159934
; GENERAL INFORMATION:
; APPLICANT: Pescovitz, Ora H.
; TITLE OF INVENTION: USE OF GHRH-RP TO STIMULATE STEM CELL FACTOR PRODUCTION
; FILE REFERENCE: 7037-175/IU-62
; CURRENT APPLICATION NUMBER: US/08/777,708C
; CURRENT FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: US 60/008,933
; PRIOR FILING DATE: 1995-12-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-08-777-708C-5

Query Match 12.0%; Score 66.5; DB 3; Length 104;
Best Local Similarity 32.9%; Pred. No. 6.5;
Matches 23; Conservative 10; Mismatches 32; Indels 5; Gaps 3;

QY 7 QEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGCGARLAEBYHAKAT 66
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Db 30 QAKLSKL-EELSDK-----IDELDAEIA-----KLEKDVDFKNSDGEQACQYLAAG 76
| | | | | | | | | | : | | | : | | : | | : | | |
QY 67 EHLSTLSEKAKPALEDLRQGL 87
| | | | | | | | | | : | | | : | | : | | : | | |
Db 77 EDLIAKKAEELEKAEADLKKAV 97

RESULT 13
US-08-893-042-4
; Sequence 4, Application US/08893042
; Patent No. 5906923
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL ATPASE INHIBITOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,042
; FILING DATE: Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0134 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 162713

Query Match 11.2%; Score 62.5; DB 2; Length 109;
Best Local Similarity 27.5%; Pred. No. 19;
Matches 22; Conservative 13; Mismatches 36; Indels 9; Gaps 2;

QY 14 GEEMRDRARAHVDALR-----THLAPYSDELQRQLAARLEALKENGCGARLAEBYHAKA 65
| | | | | | | | | | : | | | : | | : | | : | | |
Db 26 GSESGDNVRSSAGAVRDAGGAFGKREQAEERYFRARAKEQLAALKKHENEIS-HHAK 84
| | | | | | | | | | : | | | : | | : | | : | | |

QY 66 TEHLSTLSEKAKPALEDLRQ 85
| | | | | | | | | | : | | | : | | : | | : | | |
Db 85 IERLQKEIERHKQSIKKLKQ 104

RESULT 14
US-09-147-875A-5
; Sequence 5, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.

; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-5

Query Match 10.9%; Score 60.5; DB 4; Length 100;
Best Local Similarity 26.7%; Pred. No. 28;
Matches 23; Conservative 15; Mismatches 35; Indels 13; Gaps 3;

QY 2 KLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGCGARLA 61
: | | | | | | | | | | : | | | : | | : | | : | | |
Db 24 ELDAKQAKLSKL-EELSDK----IDELDAEIA-----KLEKDVDFKNSDGEQAGQY 70
| | | | | | | | | | : | | | : | | : | | : | | |

QY 62 HAKATEHLSTLSEKAKPALEDLRQGL 87
| | | | | | | | | | : | | | : | | : | | : | | |
Db 71 LAAAEEDLIAKKAEELEQTEADLKKAV 96

RESULT 15
US-08-182-175A-57
; Sequence 57, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-182-175A-57

Query Match 10.7%; Score 59.5; DB 1; Length 77;
Best Local Similarity 25.3%; Pred. No. 26;
Matches 22; Conservative 15; Mismatches 27; Indels 23; Gaps 3;

| | | | |
|----|---|---|----|
| QY | 1 | QKLHELQEKLSPLEE--MRDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGGA | 57 |
| Dd | 3 | EKLKAMEEKLKAMEEKLKAMEEKLKA-----NEEKLKAMEEKLK----- | 48 |

QY 58 LAEYHAKATEHLSTLSEKAKPALEDLR 84
| | | | | : | | | | :
Db 49 -----XMEEKLXWMEEKLKKWMEEKLK 69

Search completed: December 21, 2004, 11:55:49
Job time : 39 secs